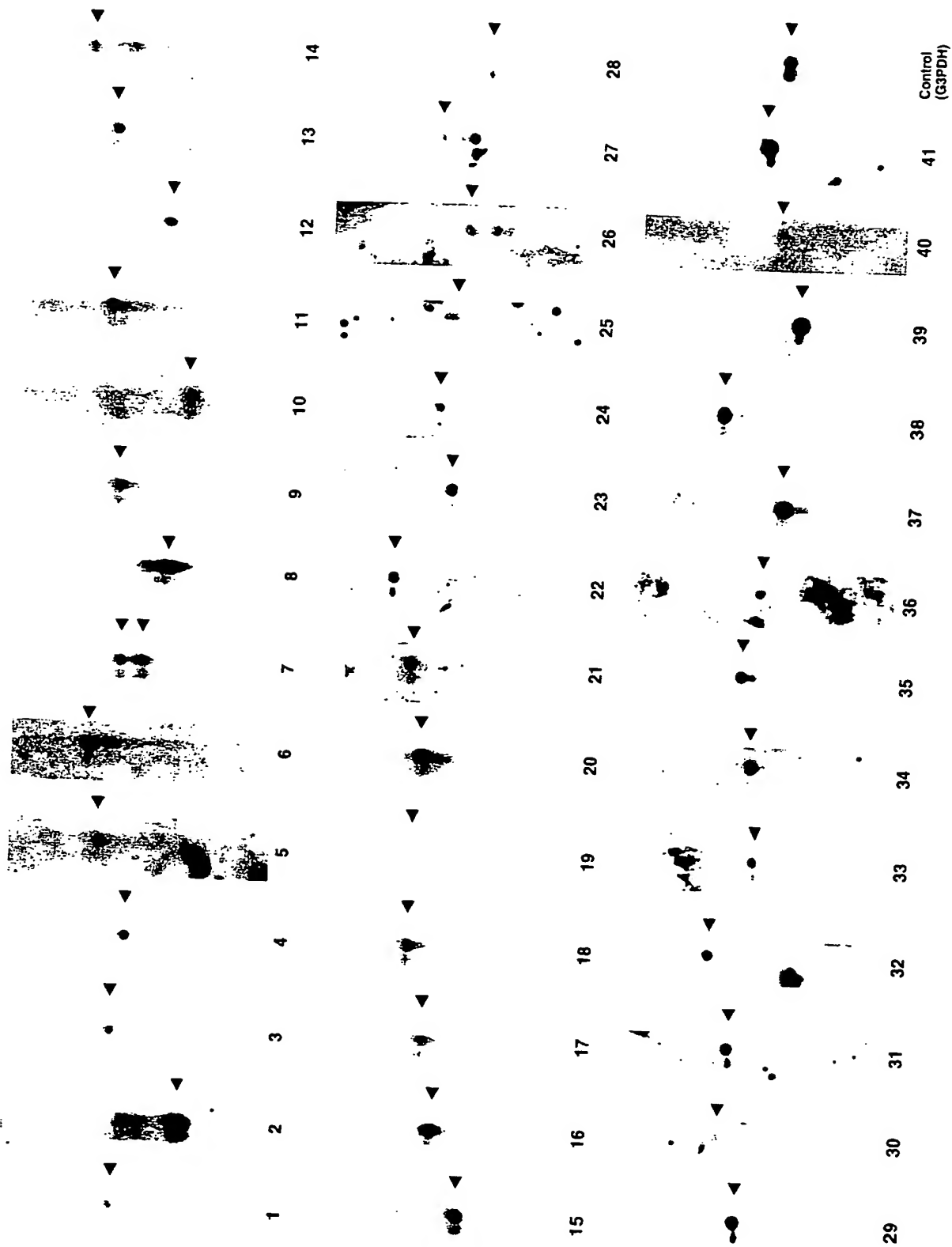
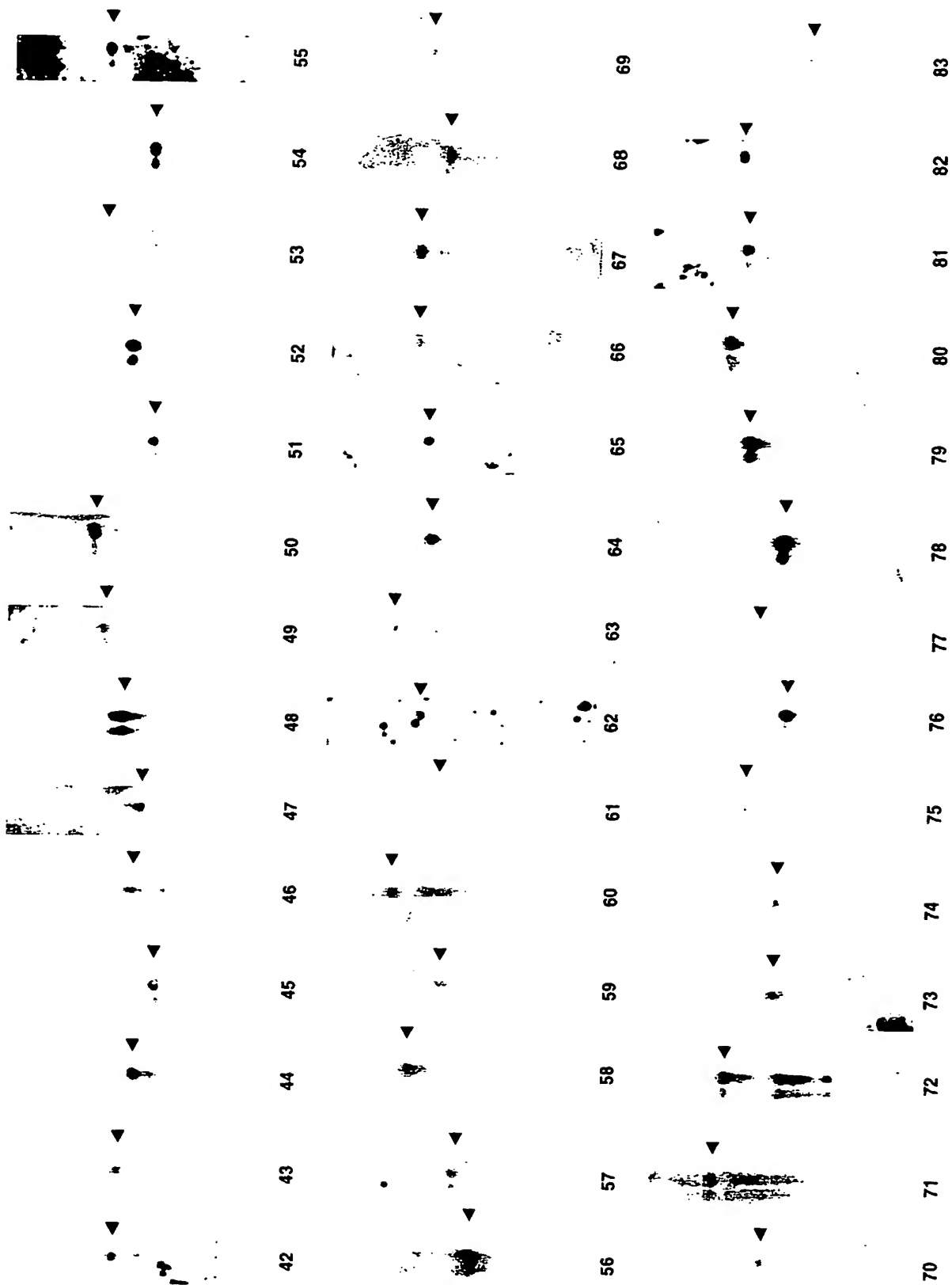


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☒ 2



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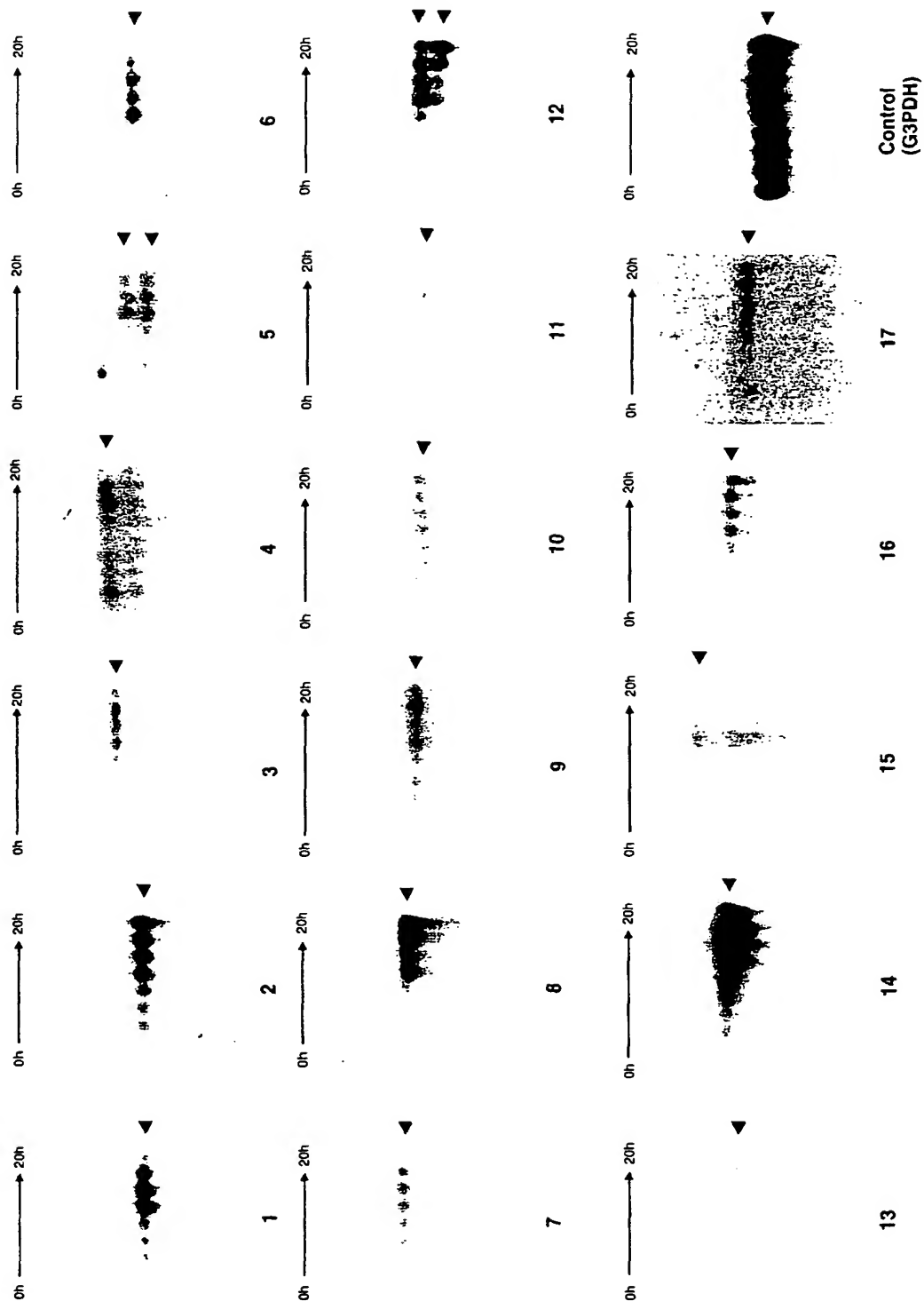


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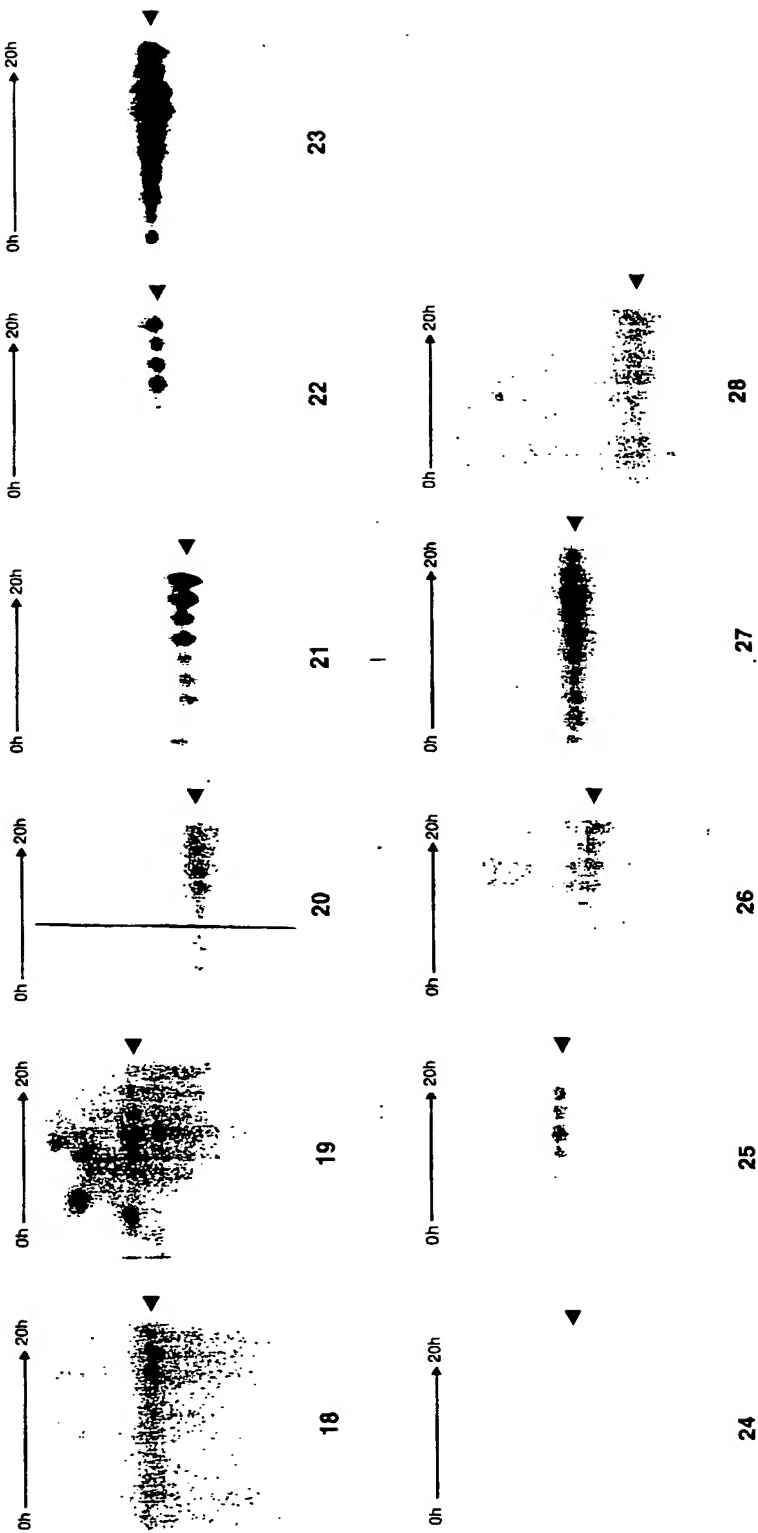


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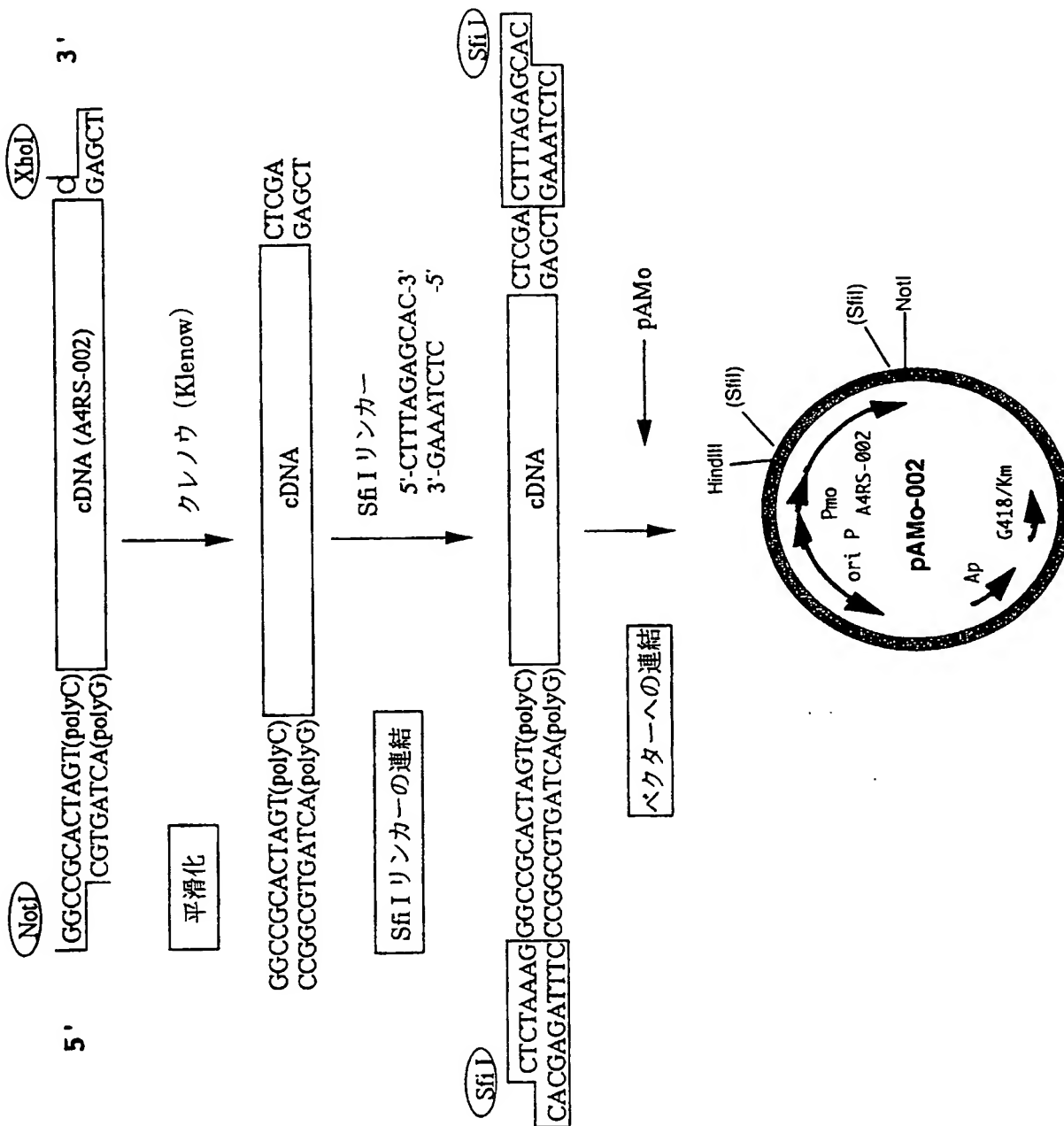


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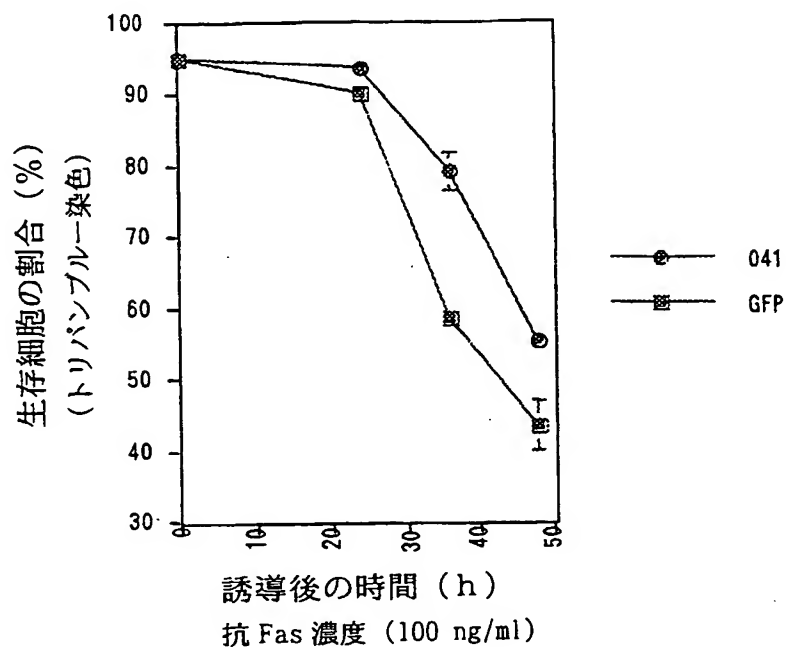
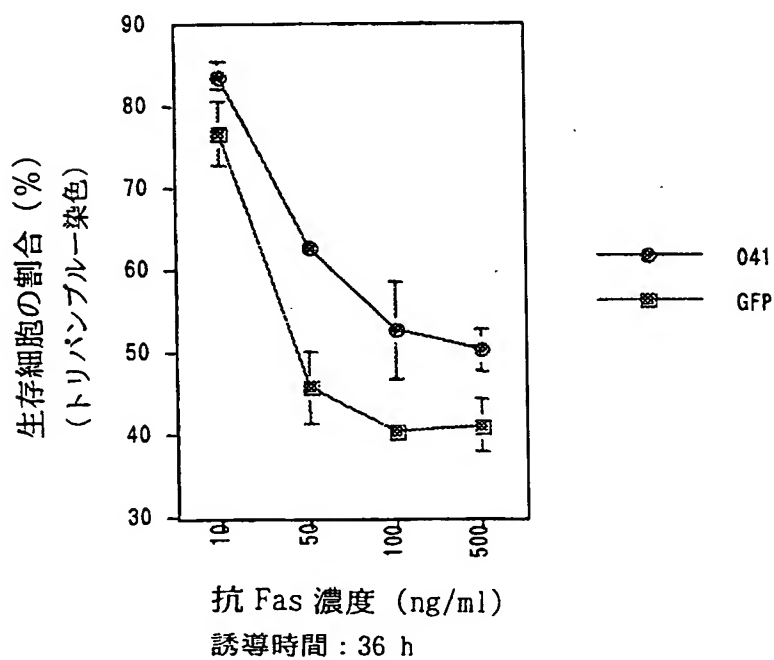
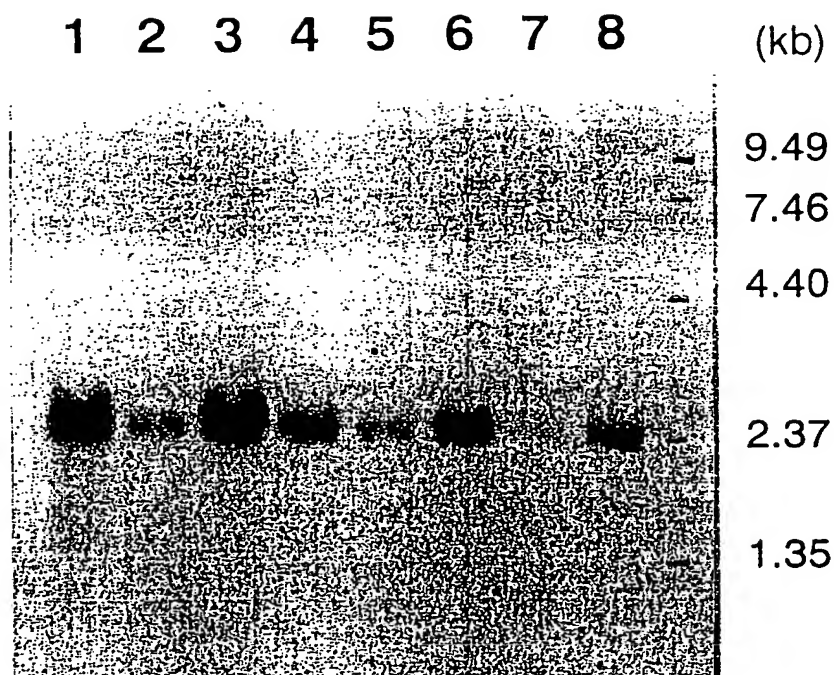


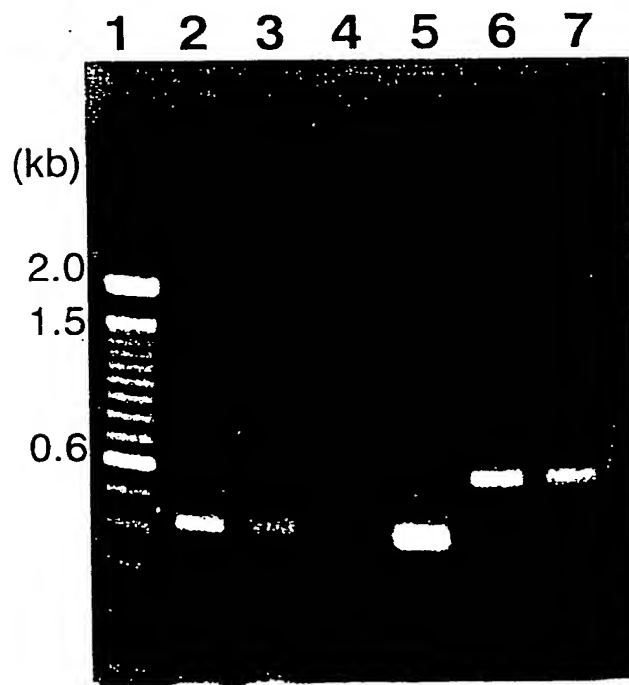
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☒ 7A



☒ 7B



☒ 08

A4RS-041
LFG

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Ile Leu Gln Ala Gly Cys

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Glu Pro Val Pro Glu Gly Asp Gly His Trp Gln Gly Arg Val Arg Thr
245 250 255

Leu Leu Glu Cys Gly Val Arg Pro Gly His Gly Asp Phe Leu Phe Thr
260 265 270

Gly His Met His Phe Gly Glu Ala Arg Leu Gly Cys Ala Pro Arg Phe
275 280 285

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<211> 2820

<212> DNA

<213> Homo sapiens

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<222> (49).. (2664)

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Gly Ala Ala Gln Glu Leu Gln Ala Lys Leu Ala Glu Ile Gly Ala Pro

5

10

15

atc cag ggt aat cgc gag gag ctg gtg gag cgg ctg cag agc tac acc 153

Ile Gln Gly Asn Arg Glu Glu Leu Val Glu Arg Leu Gln Ser Tyr Thr

20

25

30

35

cgc cag act ggc atc gtg ctg aat cgg ccg gtt ttg aga ggg gaa gat 201

Arg Gln Thr Gly Ile Val Leu Asn Arg Pro Val Leu Arg Gly Glu Asp

40

45

50

ggg gac aaa gcc gct cca cct ccc atg tcg gca cag ctc cct gga att 249

Gly Asp Lys Ala Ala Pro Pro Pro Met Ser Ala Gln Leu Pro Gly Ile

55

60

65

ccc atg cca cca cca cct ttg gga ctc ccc cct ctg cag cct cct ccg 297

Pro Met Pro Pro Pro Pro Leu Gly Leu Pro Pro Leu Gln Pro Pro Pro

70

75

80

cca ccc cca cca cct cca cca ggc ctt ggc ctt ggc ttt cct atg gcc 345

Pro Pro Pro Pro Pro Pro Pro Gly Leu Gly Leu Gly Phe Pro Met Ala
 85 90 95
 cac cca cca aat ttt ggg ccc ccg cct cct ctc cgt gtg ggt gag cca 393
 His Pro Pro Asn Leu Gly Pro Pro Pro Pro Leu Arg Val Gly Glu Pro
 100 105 110 115
 gtg gca ctg tca gag gag gag cgg ctg aag ttg gct cag cag cag gcg 441
 Val Ala Leu Ser Glu Glu Glu Arg Leu Lys Leu Ala Gln Gln Gln Ala
 120 125 130
 gca ttg ctg atg cag cag gag gag cgt gcc aag cag cag gga gat cat 489
 Ala Leu Leu Met Gln Gln Glu Glu Arg Ala Lys Gln Gln Gly Asp His
 135 140 145
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 Ser Leu Lys Glu His Glu Leu Leu Glu Gln Gln Lys Arg Ala Ala Val
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 Val Pro Arg Pro Pro Gln Asp Met Gly Gln Ile Gly Val Arg Thr Pro
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 Thr Val Leu Pro Met Gly Ala Pro Val Pro Arg Pro Arg Gly Pro Pro
 215 220 225

ccg ccc cct gga gat gag aac aga gag atg gat gac ccc tct gtg ggc 777
 Pro Pro Pro Gly Asp Glu Asn Arg Glu Met Asp Asp Pro Ser Val Gly
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 ccc aag atc ccc cag gct ttg gag aag atc ctg cag ctg aag gag agc 825
 Pro Lys Ile Pro Gln Ala Leu Glu Lys Ile Leu Gln Leu Lys Glu Ser
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 Arg Gln Glu Glu Met Asn Ser Gln Gln Glu Glu Glu Met Glu Thr
 260 265 270 275
 gat gct cgc tcg tcc ctg ggc cag tca gcg tca gag act gag gag gac 921
 Asp Ala Arg Ser Ser Leu Gly Gln Ser Ala Ser Glu Thr Glu Glu Asp
 280 285 290
 aca gtg tcc gta tct aaa aag gag aaa aac cgg aag cgt agg aac cga 969
 Thr Val Ser Val Ser Lys Lys Glu Lys Asn Arg Lys Arg Arg Asn Arg
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 aag aag aag aaa aag ccc cag cgg gtg cga ggg gtg tcc tct gag agc 1017
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 Ser Gly Asp Arg Glu Lys Asp Ser Thr Arg Ser Arg Gly Ser Asp Ser
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 Pro Ala Ala Asp Val Glu Ile Glu Tyr Val Thr Glu Glu Pro Glu Ile
 340 345 350 355
 tac gag ccc aac ttt atc ttc ttt aag agg atc ttt gag gct ttt aag 1161
 Tyr Glu Pro Asn Phe Ile Phe Phe Lys Arg Ile Phe Glu Ala Phe Lys
 360 365 370

ctc act gat gat gtg aag aag gag aaa gag aaa gag cca gag aaa ctt 1209
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 375 380 385
 gac aaa ctg gag aac tct gca gcc ccc aag aag aag gga ttt gaa gag 1257
 Asp Lys Leu Glu Asn Ser Ala Ala Pro Lys Lys Lys Gly Phe Glu Glu
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 gag cac aag gac agt gat gat gac agc agt gat gac gag cag gaa aag 1305
 Glu His Lys Asp Ser Asp Asp Asp Ser Ser Asp Asp Glu Gln Glu Lys
 405 410 415
 aag cca gaa gcc ccc aag ctg tcc aag aag aag ttg cgc cga atg aac 1353
 Lys Pro Glu Ala Pro Lys Leu Ser Lys Lys Lys Leu Arg Arg Met Asn
 420 425 430 435
 cgc ttc act gtg gct gaa ctc aag cag ctg gtg gct cgg ccc gat gtc 1401
 Arg Phe Thr Val Ala Glu Leu Lys Gln Leu Val Ala Arg Pro Asp Val
 440 445 450
 gtg gag atg cac gat gtg aca gcg cag gac cct aag ctc ttg gtt cac 1449
 Val Glu Met His Asp Val Thr Ala Gln Asp Pro Lys Leu Leu Val His
 455 460 465
 ctc aag gcc act cgg aac tct gtg cct gtg cca cgc cac tgg tgt ttt 1497
 Leu Lys Ala Thr Arg Asn Ser Val Pro Val Pro Arg His Trp Cys Phe
 470 475 480
 aag cgc aaa tac ctg cag ggc aaa cgg ggc att gag aag ccc ccc ttc 1545
 Lys Arg Lys Tyr Leu Gln Gly Lys Arg Gly Ile Glu Lys Pro Pro Phe
 485 490 495
 gag ctg cca gac ttc atc aaa cgc aca ggc atc cag gag atg cga gag 1593
 Glu Leu Pro Asp Phe Ile Lys Arg Thr Gly Ile Gln Glu Met Arg Glu

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gcc ctg cag gag aag gaa gaa cag aag acc atg aag tca aaa atg cga				1641
Ala Leu Gln Glu Lys Glu Glu Gln Lys Thr Met Lys Ser Lys Met Arg				
	520	525	530	
gag aaa gtt cgg cct aag atg ggc aaa att gac atc gac tac cag aaa				1689
Glu Lys Val Arg Pro Lys Met Gly Lys Ile Asp Ile Asp Tyr Gln Lys				
	535	540	545	
ctg cat gat gcc ttc ttc aag tgg cag acc aag cca aag ctg acc atc				1737
Leu His Asp Ala Phe Phe Lys Trp Gln Thr Lys Pro Lys Leu Thr Ile				
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cat ggg gac ctg tac tat gag ggg aag gag ttc gag aca cga ctg aag				1785
His Gly Asp Leu Tyr Tyr Glu Gly Lys Glu Phe Glu Thr Arg Leu Lys				
	565	570	575	
gag aag aag cca gga gat ctg tct gat gag cta agg att tcc ttg ggg				1833
Glu Lys Lys Pro Gly Asp Leu Ser Asp Glu Leu Arg Ile Ser Leu Gly				
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atg cca gta gga cca aat gcc cac aag gtc cct ccc cca tgg ctg att				1881
Met Pro Val Gly Pro Asn Ala His Lys Val Pro Pro Pro Trp Leu Ile				
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gcc atg cag cga tat gga cca ccc cca tcg tat ccc aac ctg aaa atc				1929
Ala Met Gln Arg Tyr Gly Pro Pro Pro Ser Tyr Pro Asn Leu Lys Ile				
	615	620	625	
cct ggg ctg aac tcg ccc atc cct gag agc tgt tcc ttt ggg tac cat				1977
Pro Gly Leu Asn Ser Pro Ile Pro Glu Ser Cys Ser Phe Gly Tyr His				
	630	635	640	
gct ggt ggc tgg ggc aaa cct cca gtg gat gag act ggg aaa ccg ctc				2025
Ala Gly Gly Trp Gly Lys Pro Pro Val Asp Glu Thr Gly Lys Pro Leu				

645	650	655	
tal ggg gac gtg ttt gga acc aat gct gct gaa tit cag acc aag act	2073		
Tyr Gly Asp Val Phe Gly Thr Asn Ala Ala Glu Phe Gln Thr Lys Thr			
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gag gaa gaa gag att gat cgg acc cct tgg ggg gaa ctg gaa cca tct	2121		
Glu Glu Glu Glu Ile Asp Arg Thr Pro Trp Gly Glu Leu Glu Pro Ser			
680	685	690	
gat gaa gaa tcc tca gaa gaa gag gaa gag gaa gaa agt gat gaa gac	2169		
Asp Glu Glu Ser Ser Glu Glu Glu Glu Glu Glu Glu Ser Asp Glu Asp			
695	700	705	
aaa cca gat gag aca ggc ttt att acc cct gca gac agt ggc ctt atc	2217		
Lys Pro Asp Glu Thr Gly Phe Ile Thr Pro Ala Asp Ser Gly Leu Ile			
710	715	720	
act cct gga ggc ttt tca tca gtg cct gct gga atg gag acc cct gaa	2265		
Thr Pro Gly Gly Phe Ser Ser Val Pro Ala Gly Met Glu Thr Pro Glu			
725	730	735	
ctc att gag ctg agg aag aag aag att gag gag gcg atg gac gga agt	2313		
Leu Ile Glu Leu Arg Lys Lys Lys Ile Glu Glu Ala Met Asp Gly Ser			
740	745	750	755
gag aca cct cag ctc ttc act gtg ttg cca gag aag aga aca gcc act	2361		
Glu Thr Pro Gln Leu Phe Thr Val Leu Pro Glu Lys Arg Thr Ala Thr			
760	765	770	
gtt gga ggg gcc atg atg gga tca acc cac att tat gac atg tcc acg	2409		
Val Gly Gly Ala Met Met Gly Ser Thr His Ile Tyr Asp Met Ser Thr			
775	780	785	
gtt atg agc cgg aag ggc ccg gct cct gag ctg caa ggt gtg gaa gtg	2457		

Val Met Ser Arg Lys Gly Pro Ala Pro Glu Leu Gln Gly Val Glu Val
 790 795 800
 gcg ctg gcg cct gaa gag ttg gag ctg gat cct atg gcc atg acc cag 2505
 Ala Leu Ala Pro Glu Glu Leu Glu Leu Asp Pro Met Ala Met Thr Gln
 805 810 815
 aag tat gag gag cat gtg cgg gag cag cag gct caa gta gag aag gag 2553
 Lys Tyr Glu Glu His Val Arg Glu Gln Gln Ala Gln Val Glu Lys Glu
 820 825 830 835
 gac ttc agt gac atg gtg gct gag cac gct gcc aaa cag aag caa aaa 2601
 Asp Phe Ser Asp Met Val Ala Glu His Ala Ala Lys Gln Lys Gln Lys
 840 845 850
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 Lys Arg Lys Ala Gln Pro Gln Asp Ser Arg Gly Gly Ser Lys Lys Tyr
 855 860 865
 aag gag ttc aag ttt taggtcccct cacactagcc ctttttttgg ccctacgtct 2704
 Lys Glu Phe Lys Phe
 870
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35 40 45
Gly Glu Asp Gly Asp Lys Ala Ala Pro Pro Pro Met Ser Ala Gln Leu
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Pro Gly Ile Pro Met Pro Pro Pro Pro Leu Gly Leu Pro Pro Leu Gln
65 70 75 80
Pro Pro Pro Pro Pro Pro Pro Pro Pro Pro Gly Leu Gly Leu Gly Phe
85 90 95
Pro Met Ala His Pro Pro Asn Leu Gly Pro Pro Pro Pro Leu Arg Val
100 105 110
Gly Glu Pro Val Ala Leu Ser Glu Glu Glu Arg Leu Lys Leu Ala Gln
115 120 125
Gln Gln Ala Ala Leu Leu Met Gln Gln Glu Glu Arg Ala Lys Gln Gln
130 135 140
Gly Asp His Ser Leu Lys Glu His Glu Leu Leu Glu Gln Gln Lys Arg
145 150 155 160
Ala Ala Val Leu Leu Glu Gln Glu Arg Gln Gln Glu Ile Ala Lys Met
165 170 175
Gly Thr Pro Val Pro Arg Pro Pro Gln Asp Met Gly Gln Ile Gly Val
180 185 190
Arg Thr Pro Leu Gly Pro Arg Val Ala Ala Pro Val Gly Pro Val Gly
195 200 205
Pro Thr Pro Thr Val Leu Pro Met Gly Ala Pro Val Pro Arg Pro Arg
210 215 220
Gly Pro Pro Pro Pro Pro Gly Asp Glu Asn Arg Glu Met Asp Asp Pro

225 230 235 240
Ser Val Gly Pro Lys Ile Pro Gln Ala Leu Glu Lys Ile Leu Gln Leu
 245 250 255
Lys Glu Ser Arg Gln Glu Glu Met Asn Ser Gln Gln Glu Glu Glu Glu
 260 265 270
Met Glu Thr Asp Ala Arg Ser Ser Leu Gly Gln Ser Ala Ser Glu Thr
 275 280 285
Glu Glu Asp Thr Val Ser Val Ser Lys Lys Glu Lys Asn Arg Lys Arg
 290 295 300
Arg Asn Arg Lys Lys Lys Lys Lys Pro Gln Arg Val Arg Gly Val Ser
305 310 315 320
Ser Glu Ser Ser Gly Asp Arg Glu Lys Asp Ser Thr Arg Ser Arg Gly
 325 330 335
Ser Asp Ser Pro Ala Ala Asp Val Glu Ile Glu Tyr Val Thr Glu Glu
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Pro Glu Ile Tyr Glu Pro Asn Phe Ile Phe Phe Lys Arg Ile Phe Glu
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Ala Phe Lys Leu Thr Asp Asp Val Lys Lys Glu Lys Glu Lys Glu Pro
 370 375 380
Glu Lys Leu Asp Lys Leu Glu Asn Ser Ala Ala Pro Lys Lys Lys Gly
385 390 395 400
Phe Glu Glu Glu His Lys Asp Ser Asp Asp Asp Ser Ser Asp Asp Glu
 405 410 415
Gln Glu Lys Lys Pro Glu Ala Pro Lys Leu Ser Lys Lys Lys Leu Arg
 420 425 430
Arg Met Asn Arg Phe Thr Val Ala Glu Leu Lys Gln Leu Val Ala Arg

435 440 445
Pro Asp Val Val Glu Met His Asp Val Thr Ala Gln Asp Pro Lys Leu
450 455 460
Leu Val His Leu Lys Ala Thr Arg Asn Ser Val Pro Val Pro Arg His
465 470 475 480
Trp Cys Phe Lys Arg Lys Tyr Leu Gln Gly Lys Arg Gly Ile Glu Lys
485 490 495
Pro Pro Phe Glu Leu Pro Asp Phe Ile Lys Arg Thr Gly Ile Gln Glu
500 505 510
Met Arg Glu Ala Leu Gln Glu Lys Glu Glu Gln Lys Thr Met Lys Ser
515 520 525
Lys Met Arg Glu Lys Val Arg Pro Lys Met Gly Lys Ile Asp Ile Asp
530 535 540
Tyr Gln Lys Leu His Asp Ala Phe Phe Lys Trp Gln Thr Lys Pro Lys
545 550 555 560
Leu Thr Ile His Gly Asp Leu Tyr Tyr Glu Gly Lys Glu Phe Glu Thr
565 570 575
Arg Leu Lys Glu Lys Lys Pro Gly Asp Leu Ser Asp Glu Leu Arg Ile
580 585 590
Ser Leu Gly Met Pro Val Gly Pro Asn Ala His Lys Val Pro Pro Pro
595 600 605
Trp Leu Ile Ala Met Gln Arg Tyr Gly Pro Pro Pro Ser Tyr Pro Asn
610 615 620
Leu Lys Ile Pro Gly Leu Asn Ser Pro Ile Pro Glu Ser Cys Ser Phe
625 630 635 640
Gly Tyr His Ala Gly Gly Trp Gly Lys Pro Pro Val Asp Glu Thr Gly
645 650 655

Lys Pro Leu Tyr Gly Asp Val Phe Gly Thr Asn Ala Ala Glu Phe Gln
 660 665 670
 Thr Lys Thr Glu Glu Glu Glu Ile Asp Arg Thr Pro Trp Gly Glu Leu
 675 680 685
 Glu Pro Ser Asp Glu Glu Ser Ser Glu Glu Glu Glu Glu Glu Ser
 690 695 700
 Asp Glu Asp Lys Pro Asp Glu Thr Gly Phe Ile Thr Pro Ala Asp Ser
 705 710 715 720
 Gly Leu Ile Thr Pro Gly Gly Phe Ser Ser Val Pro Ala Gly Met Glu
 725 730 735
 Thr Pro Glu Leu Ile Glu Leu Arg Lys Lys Lys Ile Glu Glu Ala Met
 740 745 750
 Asp Gly Ser Glu Thr Pro Gln Leu Phe Thr Val Leu Pro Glu Lys Arg
 755 760 765
 Thr Ala Thr Val Gly Gly Ala Met Met Gly Ser Thr His Ile Tyr Asp
 770 775 780
 Met Ser Thr Val Met Ser Arg Lys Gly Pro Ala Pro Glu Leu Gln Gly
 785 790 795 800
 Val Glu Val Ala Leu Ala Pro Glu Glu Leu Glu Leu Asp Pro Met Ala
 805 810 815
 Met Thr Gln Lys Tyr Glu Glu His Val Arg Glu Gln Gln Ala Gln Val
 820 825 830
 Glu Lys Glu Asp Phe Ser Asp Met Val Ala Glu His Ala Ala Lys Gln
 835 840 845
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Lys Lys Tyr Lys Glu Phe Lys Phe

865

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<211> 2433

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<222> (214).. (1146)

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 ctggtccccc gaggtctctg ccagctgac agtgttcttg gcactgctca aaggtcccag 180
 cagctggggt tccccgtcag cccgtgagcg gcc atg tcc aac ccc agc gcc cca 234

Met Ser Asn Pro Ser Ala Pro

1

5

cca cca tat gaa gac cgc aac ccc ctg tac cca ggc cct ccg ccc cct 282

Pro Pro Tyr Glu Asp Arg Asn Pro Leu Tyr Pro Gly Pro Pro Pro Pro

10

15

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ggg ggc tat ggg cag cca tct gtc ctg cca gga ggg tat cct gcc tac 330

Gly Gly Tyr Gly Gln Pro Ser Val Leu Pro Gly Gly Tyr Pro Ala Tyr

25

30

35

cct ggc tac ccg cag cct ggc tac ggt cac cct gct ggc tac cca cag 378

Pro Gly Tyr Pro Gln Pro Gly Tyr Gly His Pro Ala Gly Tyr Pro Gln

40

45

50

55

ccc atg ccc ccc acc cac ccg atg ccc atg aac tac ggc cca ggc cat 426

Pro Met Pro Pro Thr His Pro Met Pro Met Asn Tyr Gly Pro Gly His
 60 65 70
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 Gly Tyr Asp Gly Glu Glu Arg Ala Val Ser Asp Ser Phe Gly Pro Gly
 75 80 85
 gag tgg gat gac cgg aaa gtg cga cac act ttt atc cga aag gtt tac 522
 Glu Trp Asp Asp Arg Lys Val Arg His Thr Phe Ile Arg Lys Val Tyr
 90 95 100
 tcc atc atc tcc gtg cag ctg ctc atc act gtg gcc atc att gct atc 570
 Ser Ile Ile Ser Val Gln Leu Leu Ile Thr Val Ala Ile Ile Ala Ile
 105 110 115
 ttc acc ttt gtg gaa cct gtc agc gcc ttt gtg agg aga aat gtg gct 618
 Phe Thr Phe Val Glu Pro Val Ser Ala Phe Val Arg Arg Asn Val Ala
 120 125 130 135
 gtc tac tac gtg tcc tat gct gtc ttc gtt gtc acc tac ctg atc ctt 666
 Val Tyr Tyr Val Ser Tyr Ala Val Phe Val Val Thr Tyr Leu Ile Leu
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 ctg acc ctt ttt act ttt gcc atg ggc ttc atg acg ggc acc att tcc 762
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 170 175 180
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 Ser Met Tyr Gln Thr Lys Ala Val Ile Ile Ala Met Ile Ile Thr Ala
 185 190 195
 gtg gla tcc att tca gtc acc atc ttc tgc ttt cag acc aag gtg gac 858

Val Val Ser Ile Ser Val Thr Ile Phe Cys Phe Gln Thr Lys Val Asp
 200 205 210 215
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 220 225 230
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 Val Thr Gly Ile Val Thr Ser Ile Val Leu Tyr Phe Gln Tyr Val Tyr
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<211> 311

<212> PRT

<213> Homo sapiens

<400> 8

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Tyr Pro Gly Pro Pro Pro Gly Gly Tyr Gly Gln Pro Ser Val Leu

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Pro Gly Gly Tyr Pro Ala Tyr Pro Gly Tyr Pro Gln Pro Gly Tyr Gly

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His Pro Ala Gly Tyr Pro Gln Pro Met Pro Pro Thr His Pro Met Pro			
50	55	60	
Met Asn Tyr Gly Pro Gly His Gly Tyr Asp Gly Glu Glu Arg Ala Val			
65	70	75	80
Ser Asp Ser Phe Gly Pro Gly Glu Trp Asp Asp Arg Lys Val Arg His			
85	90	95	
Thr Phe Ile Arg Lys Val Tyr Ser Ile Ile Ser Val Gln Leu Leu Ile			
100	105	110	
Thr Val Ala Ile Ile Ala Ile Phe Thr Phe Val Glu Pro Val Ser Ala			
115	120	125	
Phe Val Arg Arg Asn Val Ala Val Tyr Tyr Val Ser Tyr Ala Val Phe			
130	135	140	
Val Val Thr Tyr Leu Ile Leu Ala Cys Cys Gln Gly Pro Arg Arg Arg			
145	150	155	160
Phe Pro Trp Asn Ile Ile Leu Leu Thr Leu Phe Thr Phe Ala Met Gly			
165	170	175	
Phe Met Thr Gly Thr Ile Ser Ser Met Tyr Gln Thr Lys Ala Val Ile			
180	185	190	
Ile Ala Met Ile Ile Thr Ala Val Val Ser Ile Ser Val Thr Ile Phe			
195	200	205	
Cys Phe Gln Thr Lys Val Asp Phe Thr Ser Cys Thr Gly Leu Phe Cys			
210	215	220	
Val Leu Gly Ile Val Leu Leu Val Thr Gly Ile Val Thr Ser Ile Val			
225	230	235	240
Leu Tyr Phe Gln Tyr Val Tyr Trp Leu His Met Leu Tyr Ala Ala Leu			
245	250	255	

Gly Ala Ile Cys Phe Thr Leu Phe Leu Ala Tyr Asp Thr Gln Leu Val

260

265

270

Leu Gly Asn Arg Lys His Thr Ile Ser Pro Glu Asp Tyr Ile Thr Gly

275

280

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Ala Leu Gln Ile Tyr Thr Asp Ile Ile Tyr Ile Phe Thr Phe Val Leu

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<222> (86).. (2710)

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Met Pro Glu Lys Arg Pro Phe Glu Arg

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 Gly Glu Leu Asn Asp Lys Met Lys Gly Phe Tyr Arg Ser Lys Tyr Thr
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 Thr Pro Ser Gly Glu Val Arg Tyr Ala Ala Val Thr Gln Phe Glu Ala
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Leu Ser Val Glu Gly Phe Ala Val Asp Lys Met Ala Gly Glu Val Lys
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35 40 45

Ile Val Met Asn Cys Ala Asp Ile Asp Ile Ile Thr Ala Ser Tyr Ala

50 55 60

Pro Glu Gly Asp Glu Glu Ile His Ala Thr Gly Phe Asn Tyr Gln Asn

65 70 75 80

Glu Asp Glu Lys Val Thr Leu Ser Phe Pro Ser Thr Leu Gln Thr Gly

85 90 95

Thr Gly Thr Leu Lys Ile Asp Phe Val Gly Glu Leu Asn Asp Lys Met

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Lys Gly Phe Tyr Arg Ser Lys Tyr Thr Thr Pro Ser Gly Glu Val Arg

115 120 125

Tyr Ala Ala Val Thr Gln Phe Glu Ala Thr Asp Ala Arg Arg Ala Phe

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Pro Cys Trp Asp Glu Pro Ala Ile Lys Ala Thr Phe Asp Ile Ser Leu

145 150 155 160

Val Val Pro Lys Asp Arg Val Ala Leu Ser Asn Met Asn Val Ile Asp

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Arg Lys Pro Tyr Pro Asp Asp Glu Asn Leu Val Glu Val Lys Phe Ala

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Arg Thr Pro Val Met Ser Thr Tyr Leu Val Ala Phe Val Val Gly Glu

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580 585 590
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Ser Asp Leu Ser Cys Asn Leu Gly Ile Leu Ser Thr Leu Leu Ser His
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Thr Asp Phe Tyr Glu Glu Ile Gln Glu Phe Val Lys Asp Val Phe Ser
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Pro Ile Gly Glu Arg Leu Gly Trp Asp Pro Lys Pro Gly Glu Gly His
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Gly His Lys Ala Thr Leu Glu Glu Ala Arg Arg Arg Phe Lys Asp His
675 680 685
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Leu Thr Val Leu Lys His Gly Asp Gly Thr Thr Leu Asp Ile Met Leu
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Lys Leu His Lys Gln Ala Asp Met Gln Glu Glu Lys Asn Arg Ile Glu
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Arg Val Leu Gly Ala Thr Leu Leu Pro Asp Leu Ile Gln Lys Val Leu
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Thr Phe Ala Leu Ser Glu Glu Val Arg Pro Gln Asp Thr Val Ser Val
755 760 765
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770 775 780
Lys Phe Ile Lys Asp Asn Trp Glu Glu Leu Tyr Asn Arg Tyr Gln Gly
785 790 795 800
Gly Phe Leu Ile Ser Arg Leu Ile Lys Leu Ser Val Glu Gly Phe Ala
805 810 815
Val Asp Lys Met Ala Gly Glu Val Lys Ala Phe Phe Glu Ser His Pro
820 825 830
Ala Pro Ser Ala Glu Arg Thr Ile Gln Gln Cys Cys Glu Asn Ile Leu

835	840	845
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<211> 2007

<212> DNA

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<222> (1124).. (1330)

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Met Asp Lys Gln

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 Ala Phe Ser Leu Met Phe Val Leu Lys Asp Leu Ser Pro Thr Ile Phe
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gtg cgt gag gag ttt aag gag ctg aaa gcg cgc aat acc aag aag gag	506		
Val Arg Glu Glu Phe Lys Glu Leu Lys Ala Arg Asn Thr Lys Lys Glu			
110	115	120	
ggt gac ctg ata gct gct cag gct cgg ctg aag gac ctg gag gct ctg	554		
Gly Asp Leu Ile Ala Ala Gln Ala Arg Leu Lys Asp Leu Glu Ala Leu			
125	130	135	140
ctg aac tcc aag gag gcc gca ctg agc act gct ctc agt gag aag cgc	602		
Leu Asn Ser Lys Glu Ala Ala Leu Ser Thr Ala Leu Ser Glu Lys Arg			
145	150	155	
acg ctg gag ggc gag ctg cat gat ctg cgg ggc cag gtg gcc aag ctt	650		
Thr Leu Glu Gly Glu Leu His Asp Leu Arg Gly Gln Val Ala Lys Leu			
160	165	170	
gag gca gcc cta ggt gag gcc aag aag caa ctt cag gat gag atg ctg	698		
Glu Ala Ala Leu Gly Glu Ala Lys Lys Gln Leu Gln Asp Glu Met Leu			
175	180	185	
cgg cgg gtg gat gct gag aac agg ctg cag acc atg aag gag gaa ctg	746		
Arg Arg Val Asp Ala Glu Asn Arg Leu Gln Thr Met Lys Glu Glu Leu			
190	195	200	
gac ttc cag aag aac atc tac agt gag gag ctg cgt gag acc aag cgc	794		
Asp Phe Gln Lys Asn Ile Tyr Ser Glu Glu Leu Arg Glu Thr Lys Arg			
205	210	215	220
cgt cat gag acc cga ctg gtg gag att gac aat ggg aag cag cgt gag	842		
Arg His Glu Thr Arg Leu Val Glu Ile Asp Asn Gly Lys Gln Arg Glu			
225	230	235	
ttt gag agc cgg ctg gcg gat gcg ctg cag gaa ctg cgg gcc cag cat	890		
Phe Glu Ser Arg Leu Ala Asp Ala Leu Gln Glu Leu Arg Ala Gln His			

240	245	250	
gag gac cag gtg gag cag tat aag aag gag ctg gag aag act tat tct			938
Glu Asp Gln Val Glu Gln Tyr Lys Lys Glu Leu Glu Lys Thr Tyr Ser			
255	260	265	
gcc aag ctg gac aat gcc agg cag tct gct gag agg aac agc aac ctg			986
Ala Lys Leu Asp Asn Ala Arg Gln Ser Ala Glu Arg Asn Ser Asn Leu			
270	275	280	
gtg ggg gct gcc cac gag gag ctg cag cag tct cgc atc cgc atc gac			1034
Val Gly Ala Ala His Glu Glu Leu Gln Gln Ser Arg Ile Arg Ile Asp			
285	290	295	300
agc ctc tct gcc cag ctc agc cag ctc cag aag cag ctg gca gcc aag			1082
Ser Leu Ser Ala Gln Leu Ser Gln Leu Gln Lys Gln Leu Ala Ala Lys			
305	310	315	
gag gcg aag ctt cga gac ctg gag gac tca ctg gcc cgt gag cgg gac			1130
Glu Ala Lys Leu Arg Asp Leu Glu Asp Ser Leu Ala Arg Glu Arg Asp			
320	325	330	
acc agc cgg cgg ctg ctg gcg gaa aag gag cgg gag atg gcc gag atg			1178
Thr Ser Arg Arg Leu Leu Ala Glu Lys Glu Arg Glu Met Ala Glu Met			
335	340	345	
cgg gca agg atg cag cag cag ctg gac gag tac cag gag ctt ctg gac			1226
Arg Ala Arg Met Gln Gln Gln Leu Asp Glu Tyr Gln Glu Leu Leu Asp			
350	355	360	
atc aag ctg gcc ctg gac atg gag atc cac gcc tac cgc aag ctc ttg			1274
Ile Lys Leu Ala Leu Asp Met Glu Ile His Ala Tyr Arg Lys Leu Leu			
365	370	375	380
gag ggc gag gag gag agg cta cgc ctg tcc ccc agc cct acc tcg cag			1322

Glu Gly Glu Glu Glu Arg Leu Arg Leu Ser Pro Ser Pro Thr Ser Gln
 385 390 395
 cgc agc cgt ggc cgt gct tcc tct cac tca tcc cag aca cag ggt ggg 1370
 Arg Ser Arg Gly Arg Ala Ser Ser His Ser Ser Gln Thr Gln Gly Gly
 400 405 410
 ggc agc gtc acc aaa aag cgc aaa ctg gag tcc act gag agc cgc agc 1418
 Gly Ser Val Thr Lys Lys Arg Lys Leu Glu Ser Thr Glu Ser Arg Ser
 415 420 425
 agc ttc tca cag cac gca cgc act agc ggg cgc gtg gcc gtg gag gag 1466
 Ser Phe Ser Gln His Ala Arg Thr Ser Gly Arg Val Ala Val Glu Glu
 430 435 440
 gtg gat gag gag ggc aag ttt gtc cgg ctg cgc aac aag tcc aat gag 1514
 Val Asp Glu Glu Gly Lys Phe Val Arg Leu Arg Asn Lys Ser Asn Glu
 445 450 455 460
 gac cag tcc atg ggc aat tgg cag atc aag cgc cag aat gga gat gat 1562
 Asp Gln Ser Met Gly Asn Trp Gln Ile Lys Arg Gln Asn Gly Asp Asp
 465 470 475
 ccc ttg ctg act tac cgg ttc cca cca aag ttc acc ctg aag gct ggg 1610
 Pro Leu Leu Thr Tyr Arg Phe Pro Pro Lys Phe Thr Leu Lys Ala Gly
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 Gln Val Val Thr Ile Trp Ala Ala Gly Ala Gly Ala Thr His Ser Pro
 495 500 505
 cct acc gac ctg gtg tgg aag gca cag aac acc tgg ggc tgc ggg aac 1706
 Pro Thr Asp Leu Val Trp Lys Ala Gln Asn Thr Trp Gly Cys Gly Asn
 510 515 520
 agc ctg cgt acg gct ctc atc aac tcc act ggg gaa gaa gtg gcc atg 1754

Ser Leu Arg Thr Ala Leu Ile Asn Ser Thr Gly Glu Glu Val Ala Met
 525 530 535 540
 cgc aag ctg gtg cgc tca gtg act gtg gtt gag gac gac gag gat gag 1802
 Arg Lys Leu Val Arg Ser Val Thr Val Val Glu Asp Asp Glu Asp Glu
 545 550 555
 gat gga gat gac ctg ctc cat cac cac cac gtg agt ggt agc cgc cgc 1850
 Asp Gly Asp Asp Leu Leu His His His His Val Ser Gly Ser Arg Arg
 560 565 570
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<210> 14

<211> 572

<212> PRT

<213> Homo sapiens

<400> 14

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 Ser Ser Thr Pro Leu Ser Pro Thr Arg Ile Thr Arg Leu Gln Glu Lys
 20 25 30
 Glu Asp Leu Gln Glu Leu Asn Asp Arg Leu Ala Val Tyr Ile Asp Arg
 35 40 45
 Val Arg Ser Leu Glu Thr Glu Asn Ala Gly Leu Arg Leu Arg Ile Thr
 50 55 60
 Glu Ser Glu Glu Val Val Ser Arg Glu Val Ser Gly Ile Lys Ala Ala
 65 70 75 80
 Tyr Glu Ala Glu Leu Gly Asp Ala Arg Lys Thr Leu Asp Ser Val Ala

	85	90	95
Lys Glu Arg Ala Arg Leu Gln Leu Glu Leu Ser Lys Val Arg Glu Glu			
100	105	110	
Phe Lys Glu Leu Lys Ala Arg Asn Thr Lys Lys Glu Gly Asp Leu Ile			
115	120	125	
Ala Ala Gln Ala Arg Leu Lys Asp Leu Glu Ala Leu Leu Asn Ser Lys			
130	135	140	
Glu Ala Ala Leu Ser Thr Ala Leu Ser Glu Lys Arg Thr Leu Glu Gly			
145	150	155	160
Glu Leu His Asp Leu Arg Gly Gln Val Ala Lys Leu Glu Ala Ala Leu			
165	170	175	
Gly Glu Ala Lys Lys Gln Leu Gln Asp Glu Met Leu Arg Arg Val Asp			
180	185	190	
Ala Glu Asn Arg Leu Gln Thr Met Lys Glu Glu Leu Asp Phe Gln Lys			
195	200	205	
Asn Ile Tyr Ser Glu Glu Leu Arg Glu Thr Lys Arg Arg His Glu Thr			
210	215	220	
Arg Leu Val Glu Ile Asp Asn Gly Lys Gln Arg Glu Phe Glu Ser Arg			
225	230	235	240
Leu Ala Asp Ala Leu Gln Glu Leu Arg Ala Gln His Glu Asp Gln Val			
245	250	255	
Glu Gln Tyr Lys Lys Glu Leu Glu Lys Thr Tyr Ser Ala Lys Leu Asp			
260	265	270	
Asn Ala Arg Gln Ser Ala Glu Arg Asn Ser Asn Leu Val Gly Ala Ala			
275	280	285	
His Glu Glu Leu Gln Gln Ser Arg Ile Arg Ile Asp Ser Leu Ser Ala			

290	295	300	
Gln Leu Ser Gln Leu Gln Lys Gln Leu Ala Ala Lys Glu Ala Lys Leu			
305	310	315	320
Arg Asp Leu Glu Asp Ser Leu Ala Arg Glu Arg Asp Thr Ser Arg Arg			
	325	330	335
Leu Leu Ala Glu Lys Glu Arg Glu Met Ala Glu Met Arg Ala Arg Met			
	340	345	350
Gln Gln Gln Leu Asp Glu Tyr Gln Glu Leu Leu Asp Ile Lys Leu Ala			
	355	360	365
Leu Asp Met Glu Ile His Ala Tyr Arg Lys Leu Leu Glu Gly Glu Glu			
	370	375	380
Glu Arg Leu Arg Leu Ser Pro Ser Pro Thr Ser Gln Arg Ser Arg Gly			
385	390	395	400
Arg Ala Ser Ser His Ser Ser Gln Thr Gln Gly Gly Gly Ser Val Thr			
	405	410	415
Lys Lys Arg Lys Leu Glu Ser Thr Glu Ser Arg Ser Ser Phe Ser Gln			
	420	425	430
His Ala Arg Thr Ser Gly Arg Val Ala Val Glu Glu Val Asp Glu Glu			
	435	440	445
Gly Lys Phe Val Arg Leu Arg Asn Lys Ser Asn Glu Asp Gln Ser Met			
	450	455	460
Gly Asn Trp Gln Ile Lys Arg Gln Asn Gly Asp Asp Pro Leu Leu Thr			
465	470	475	480
Tyr Arg Phe Pro Pro Lys Phe Thr Leu Lys Ala Gly Gln Val Val Thr			
	485	490	495
Ile Trp Ala Ala Gly Ala Gly Ala Thr His Ser Pro Pro Thr Asp Leu			
	500	505	510

Val Trp Lys Ala Gln Asn Thr Trp Gly Cys Gly Asn Ser Leu Arg Thr

515

520

525

Ala Leu Ile Asn Ser Thr Gly Glu Glu Val Ala Met Arg Lys Leu Val

530

535

540

Arg Ser Val Thr Val Val Glu Asp Asp Glu Asp Glu Asp Gly Asp Asp

545

550

555

560

Leu Leu His His His His Val Ser Gly Ser Arg Arg

565

570

<210> 15

<211> 2865

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (240).. (1475)

<400> 15

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cgcccccaac tgaagctgca tctcaaagcc gaagattcca gcagcccagg ggatttcaaa 120

gagctcagac tcagaggaac atctgcggag agacccccga agccctctcc agggcagicc 180

tcatccagac gctccgltag tgcagacagg agcgcgcagt ggccccggct cgccgcgcc 239

atg gag cgg atc ccc agc gcg caa cca ccc ccc gcc tgc ctg ccc aaa 287

Met Glu Arg Ile Pro Ser Ala Gln Pro Pro Pro Ala Cys Leu Pro Lys

1

5

10

15

gca ccg gga ctg gag cac cga gac cta cca ggg atg tac cct gcc cac 335

Ala Pro Gly Leu Glu His Arg Asp Leu Pro Gly Met Tyr Pro Ala His

20

25

30

atg tac caa gtg tac aag tca aga cgg gga ata aag cgg agc gag gac 383
 Met Tyr Gln Val Tyr Lys Ser Arg Arg Gly Ile Lys Arg Ser Glu Asp
 35 40 45
 agc aag gag acc tac aaa ttg ccg cac cgg ctc ttc gag aaa aag aga 431
 Ser Lys Glu Thr Tyr Lys Leu Pro His Arg Leu Phe Glu Lys Lys Arg
 50 55 60
 cgt gac cgg att aac gag tgc atc gcc cag ctg aag gat ctc cta ccc 479
 Arg Asp Arg Ile Asn Glu Cys Ile Ala Gln Leu Lys Asp Leu Leu Pro
 65 70 75 80
 gaa cat ctc aaa ctt aca act ttg ggt cac ttg gaa aaa gca gtg gtt 527
 Glu His Leu Lys Leu Thr Thr Leu Gly His Leu Glu Lys Ala Val Val
 85 90 95
 ctt gaa ctt acc ttg aag cat glg aaa gca cta aca aac cta att gat 575
 Leu Glu Leu Thr Leu Lys His Val Lys Ala Leu Thr Asn Leu Ile Asp
 100 105 110
 cag cag cag cag aaa atc att gcc ctg cag agt ggt tta caa gct ggt 623
 Gln Gln Gln Gln Lys Ile Ile Ala Leu Gln Ser Gly Leu Gln Ala Gly
 115 120 125
 gag ctg tca ggg aga aat gtc gaa aca ggt caa gag atg ttc tgc tca 671
 Glu Leu Ser Gly Arg Asn Val Glu Thr Gly Gln Glu Met Phe Cys Ser
 130 135 140
 ggt ttc cag aca tgt gcc cgg gag gtg ctt cag tat ctg gcc aag cac 719
 Gly Phe Gln Thr Cys Ala Arg Glu Val Leu Gln Tyr Leu Ala Lys His
 145 150 155 160
 gag aac act cgg gac ctg aag tct tcg cag ctt gtc acc cac ctc cac 767
 Glu Asn Thr Arg Asp Leu Lys Ser Ser Gln Leu Val Thr His Leu His

165	170	175	
cgg gfg gtc tgc gag ctg ctg cag ggt ggt acc tcc agg aag cca tca	815		
Arg Val Val Ser Glu Leu Leu Gln Gly Gly Thr Ser Arg Lys Pro Ser			
180	185	190	
gac cca gct ccc aaa gtg atg gac ttc aag gaa aaa ccc agc tct ccg	863		
Asp Pro Ala Pro Lys Val Met Asp Phe Lys Glu Lys Pro Ser Ser Pro			
195	200	205	
gcc aaa ggt tgc gaa ggt cct ggg aaa aac tgc gtg cca gtc atc cag	911		
Ala Lys Gly Ser Glu Gly Pro Gly Lys Asn Cys Val Pro Val Ile Gln			
210	215	220	
cgg act ttc gct cac tgc agt ggg gag cag agc ggc agc gac acg gac	959		
Arg Thr Phe Ala His Ser Ser Gly Glu Gln Ser Gly Ser Asp Thr Asp			
225	230	235	240
aca gac agt ggc tat gga gga gat tgc gag aag ggc gac ttg cgc agt	1007		
Thr Asp Ser Gly Tyr Gly Gly Asp Ser Glu Lys Gly Asp Leu Arg Ser			
245	250	255	
gag cag ccg tgc ttc aaa agt gac cac gga cgc agg ttc acg atg gga	1055		
Glu Gln Pro Cys Phe Lys Ser Asp His Gly Arg Arg Phe Thr Met Gly			
260	265	270	
gaa agg atc ggc gca att aag caa gag tcc gaa gaa ccc ccc aca aaa	1103		
Glu Arg Ile Gly Ala Ile Lys Gln Glu Ser Glu Glu Pro Pro Thr Lys			
275	280	285	
aag aac cgg atg cag ctt tgc gat gat gaa ggc cat ttc act agc agt	1151		
Lys Asn Arg Met Gln Leu Ser Asp Asp Glu Gly His Phe Thr Ser Ser			
290	295	300	
gac ctg atc agc tcc ccg ttc ctg ggc cca cac cca cac cag cct cct	1199		
Asp Leu Ile Ser Ser Pro Phe Leu Gly Pro His Pro His Gln Pro Pro			

305 310 315 320
 ttc tgc ctg ccc ttc tac ctg atc cca cct tca gcg act gcc tac ctg 1247
 Phe Cys Leu Pro Phe Tyr Leu Ile Pro Pro Ser Ala Thr Ala Tyr Leu
 325 330 335
 ccc atg ctg gag aag tgc tgg tat ccc acc tca glg cca glg cta tac 1295
 Pro Met Leu Glu Lys Cys Trp Tyr Pro Thr Ser Val Pro Val Leu Tyr
 340 345 350
 cca ggc ctc aac gcc tct gcc gca gcc ctc tct agc ttc atg aac cca 1343
 Pro Gly Leu Asn Ala Ser Ala Ala Ala Leu Ser Ser Phe Met Asn Pro
 355 360 365
 gac aag atc tcg gct ccc ttg ctc atg ccc cag aga ctc cct tct ccc 1391
 Asp Lys Ile Ser Ala Pro Leu Leu Met Pro Gln Arg Leu Pro Ser Pro
 370 375 380
 ttg cca gct cat ccg tcc gtc gac tct tct gtc ttg ctc caa gct ctg 1439
 Leu Pro Ala His Pro Ser Val Asp Ser Ser Val Leu Leu Gln Ala Leu
 385 390 395 400
 aag cca atc ccc cct tta aac tta gaa acc aaa gac taaactctct 1485
 Lys Pro Ile Pro Pro Leu Asn Leu Glu Thr Lys Asp
 405 410
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 caganncagg gtgtgtgtgt gtgtgtgtgt gtgtgtgtgt gtatgtgcgt gtgcgtgcac 1665
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tcaaaagagg gctttccagg gctcagctcc caaccagctg ttaggacccc acccttttgc 1965
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 ntgttncaga tgtttatttg tataattact tgattcacan agngagaaaa antgantgta 2805
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<210> 16

<211> 412

<212> PRT

<213> Homo sapiens

<400> 16

Met Glu Arg Ile Pro Ser Ala Gln Pro Pro Pro Ala Cys Leu Pro Lys

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10

15

Ala Pro Gly Leu Glu His Arg Asp Leu Pro Gly Met Tyr Pro Ala His

20

25

30

Met Tyr Gln Val Tyr Lys Ser Arg Arg Gly Ile Lys Arg Ser Glu Asp

35 40 45
Ser Lys Glu Thr Tyr Lys Leu Pro His Arg Leu Phe Glu Lys Lys Arg
50 55 60
Arg Asp Arg Ile Asn Glu Cys Ile Ala Gln Leu Lys Asp Leu Leu Pro
65 70 75 80
Glu His Leu Lys Leu Thr Thr Leu Gly His Leu Glu Lys Ala Val Val
85 90 95
Leu Glu Leu Thr Leu Lys His Val Lys Ala Leu Thr Asn Leu Ile Asp
100 105 110
Gln Gln Gln Gln Lys Ile Ile Ala Leu Gln Ser Gly Leu Gln Ala Gly
115 120 125
Glu Leu Ser Gly Arg Asn Val Glu Thr Gly Gln Glu Met Phe Cys Ser
130 135 140
Gly Phe Gln Thr Cys Ala Arg Glu Val Leu Gln Tyr Leu Ala Lys His
145 150 155 160
Glu Asn Thr Arg Asp Leu Lys Ser Ser Gln Leu Val Thr His Leu His
165 170 175
Arg Val Val Ser Glu Leu Leu Gln Gly Gly Thr Ser Arg Lys Pro Ser
180 185 190
Asp Pro Ala Pro Lys Val Met Asp Phe Lys Glu Lys Pro Ser Ser Pro
195 200 205
Ala Lys Gly Ser Glu Gly Pro Gly Lys Asn Cys Val Pro Val Ile Gln
210 215 220
Arg Thr Phe Ala His Ser Ser Gly Glu Gln Ser Gly Ser Asp Thr Asp
225 230 235 240
Thr Asp Ser Gly Tyr Gly Gly Asp Ser Glu Lys Gly Asp Leu Arg Ser
245 250 255

Glu Gln Pro Cys Phe Lys Ser Asp His Gly Arg Arg Phe Thr Met Gly
 260 265 270
 Glu Arg Ile Gly Ala Ile Lys Gln Glu Ser Glu Glu Pro Pro Thr Lys
 275 280 285
 Lys Asn Arg Met Gln Leu Ser Asp Asp Glu Gly His Phe Thr Ser Ser
 290 295 300
 Asp Leu Ile Ser Ser Pro Phe Leu Gly Pro His Pro His Gln Pro Pro
 305 310 315 320
 Phe Cys Leu Pro Phe Tyr Leu Ile Pro Pro Ser Ala Thr Ala Tyr Leu
 325 330 335
 Pro Met Leu Glu Lys Cys Trp Tyr Pro Thr Ser Val Pro Val Leu Tyr
 340 345 350
 Pro Gly Leu Asn Ala Ser Ala Ala Ala Leu Ser Ser Phe Met Asn Pro
 355 360 365
 Asp Lys Ile Ser Ala Pro Leu Leu Met Pro Gln Arg Leu Pro Ser Pro
 370 375 380
 Leu Pro Ala His Pro Ser Val Asp Ser Ser Val Leu Leu Gln Ala Leu
 385 390 395 400
 Lys Pro Ile Pro Pro Leu Asn Leu Glu Thr Lys Asp
 405 410

<210> 17

<211> 3817

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (164).. (2665)

<400> 17

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tccttaaciag ttaggaaaa cggctcaacc caccgctgcc gaa atg aag tat aag 175

Met Lys Tyr Lys

1

aat ctt atg gca agg gcc tta tat gac aat gtc cca gag tgt gcc gag 223

Asn Leu Met Ala Arg Ala Leu Tyr Asp Asn Val Pro Glu Cys Ala Glu

5

10

15

20

gaa ctg gcc ttt cgc aag gga gac atc ctg acc gtc ata gag cag aac 271

Glu Leu Ala Phe Arg Lys Gly Asp Ile Leu Thr Val Ile Glu Gln Asn

25

30

35

aca ggg gga ctg gaa gga tgg tgg ctg tgc tgc tta cac ggt cgg caa 319

Thr Gly Gly Leu Glu Gly Trp Trp Leu Cys Ser Leu His Gly Arg Gln

40

45

50

ggc att gtc cca ggc aac cgg gtg aag ctt ctg att ggt ccc atg cag 367

Gly Ile Val Pro Gly Asn Arg Val Lys Leu Leu Ile Gly Pro Met Gln

55

60

65

gag act gcc tcc agt cac gag cag cct gcc tct gga ctg atg cag cag 415

Glu Thr Ala Ser Ser His Glu Gln Pro Ala Ser Gly Leu Met Gln Gln

70

75

80

acc ttt ggc caa cag aag ctc tat caa gtg cca aac cca cag gct gct 463

Thr Phe Gly Gln Gln Lys Leu Tyr Gln Val Pro Asn Pro Gln Ala Ala

85

90

95

100

ccc cga gac acc atc tac caa gtg cca cct tcc tac caa aat cag gga 511

Pro Arg Asp Thr Ile Tyr Gln Val Pro Pro Ser Tyr Gln Asn Gln Gly
105 110 115
att tac caa gtc ccc act ggc cac ggc acc caa gaa caa gag gta tat 559
Ile Tyr Gln Val Pro Thr Gly His Gly Thr Gln Glu Gln Glu Val Tyr
120 125 130
cag gtg cca cca tca gtg cag aga agc att ggg gga acc agt ggg ccc 607
Gln Val Pro Pro Ser Val Gln Arg Ser Ile Gly Gly Thr Ser Gly Pro
135 140 145
cac gtg ggt aaa aag gtg ata acc ccc gtg agg aca ggc cat ggc tac 655
His Val Gly Lys Lys Val Ile Thr Pro Val Arg Thr Gly His Gly Tyr
150 155 160
gta tac gag tac cca tcc aga tac caa aag gat gtc tat gat atc cct 703
Val Tyr Glu Tyr Pro Ser Arg Tyr Gln Lys Asp Val Tyr Asp Ile Pro
165 170 175 180
cct tct cat acc act caa ggg gta tac gac atc cct ccc tca tca gca 751
Pro Ser His Thr Thr Gln Gly Val Tyr Asp Ile Pro Pro Ser Ser Ala
185 190 195
aaa ggc cct gtg ttt tca gtt cca gtg gga gag ata aaa cct caa ggg 799
Lys Gly Pro Val Phe Ser Val Pro Val Gly Glu Ile Lys Pro Gln Gly
200 205 210
gtg tat gac atc ccg cct aca aaa ggg gta tat gcc att ccg ccc tct 847
Val Tyr Asp Ile Pro Pro Thr Lys Gly Val Tyr Ala Ile Pro Pro Ser
215 220 225
gct tgc cgg gat gaa gca ggg cit agg gaa aaa gac tat gac ttc ccc 895
Ala Cys Arg Asp Glu Ala Gly Leu Arg Glu Lys Asp Tyr Asp Phe Pro
230 235 240
cct ccc atg aga caa gct gga agg ccg gac ctc aga ccg gag ggg gtt 943

Pro Pro Met Arg Gln Ala Gly Arg Pro Asp Leu Arg Pro Glu Gly Val
 245 250 255 260
 tat gac att cct cca acc tgc acc aag cca gca ggg aag gac ctt cat 991
 Tyr Asp Ile Pro Pro Thr Cys Thr Lys Pro Ala Gly Lys Asp Leu His
 265 270 275
 gta aaa tac aac tgt gac att cca gga gct gca gaa ccg gtg gct cga 1039
 Val Lys Tyr Asn Cys Asp Ile Pro Gly Ala Ala Glu Pro Val Ala Arg
 280 285 290
 agg cac cag agc ctg tcc ccg aat cac cca ccc ccg caa ctc gga cag 1087
 Arg His Gln Ser Leu Ser Pro Asn His Pro Pro Pro Gln Leu Gly Gln
 295 300 305
 tca gtg ggc tct cag aac gac gca tat gat gtc ccc cga ggc gtt cag 1135
 Ser Val Gly Ser Gln Asn Asp Ala Tyr Asp Val Pro Arg Gly Val Gln
 310 315 320
 ttt ctt gag cca cca gca gaa acc agt gag aaa gca aac ccc cag gaa 1183
 Phe Leu Glu Pro Pro Ala Glu Thr Ser Glu Lys Ala Asn Pro Gln Glu
 325 330 335 340
 agg gat ggt gtt tat gat gtc cct ctg cat aac ccg cca gat gct aaa 1231
 Arg Asp Gly Val Tyr Asp Val Pro Leu His Asn Pro Pro Asp Ala Lys
 345 350 355
 ggc tct cgg gac ttg gtg gat ggg atc aac cga ttg tct ttc tcc agt 1279
 Gly Ser Arg Asp Leu Val Asp Gly Ile Asn Arg Leu Ser Phe Ser Ser
 360 365 370
 aca ggc agc acc cgg agt aac atg tcc acg tct tcc acc tcc tcc aag 1327
 Thr Gly Ser Thr Arg Ser Asn Met Ser Thr Ser Ser Thr Ser Ser Lys
 375 380 385

gag tcc tca ctg tca gcc tcc cca gct cag gac aaa agg ctc ttc ctg 1375
Glu Ser Ser Leu Ser Ala Ser Pro Ala Gln Asp Lys Arg Leu Phe Leu
390 395 400
gat cca gac aca gct att gag aga ctt cag cgg ctc cag cag gcc ctt 1423
Asp Pro Asp Thr Ala Ile Glu Arg Leu Gln Arg Leu Gln Gln Ala Leu
405 410 415 420
gag atg ggt gtc tcc agc cta atg gca ctg gtc act acc gac tgg cgg 1471
Glu Met Gly Val Ser Ser Leu Met Ala Leu Val Thr Thr Asp Trp Arg
425 430 435
tgt tac gga tat atg gaa aga cac atc aat gaa ata cgc aca gca gtg 1519
Cys Tyr Gly Tyr Met Glu Arg His Ile Asn Glu Ile Arg Thr Ala Val
440 445 450
gac aag gtg gag ctg ttc ctg aag gag tac ctc cac ttt gtc aag gga 1567
Asp Lys Val Glu Leu Phe Leu Lys Glu Tyr Leu His Phe Val Lys Gly
455 460 465
gct gtt gca aat gct gcc tgc ctc ccg gaa ctc atc ctc cac aac aag 1615
Ala Val Ala Asn Ala Ala Cys Leu Pro Glu Leu Ile Leu His Asn Lys
470 475 480
atg aag cgg gag ctg caa cga gtc gaa gac tcc cac cag atc ctg agt 1663
Met Lys Arg Glu Leu Gln Arg Val Glu Asp Ser His Gln Ile Leu Ser
485 490 495 500
caa acc agc cat gac tta aat gag tgc agc tgg tcc ctg aat atc ttg 1711
Gln Thr Ser His Asp Leu Asn Glu Cys Ser Trp Ser Leu Asn Ile Leu
505 510 515
gcc atc aac aag ccc cag aac aag tgt gac gat ctg gac cgg ttt gtg 1759
Ala Ile Asn Lys Pro Gln Asn Lys Cys Asp Asp Leu Asp Arg Phe Val
520 525 530

atg glg gca aag acg gtg ccc gat gac gcc aag cag ctc acc aca acc 1807
 Met Val Ala Lys Thr Val Pro Asp Asp Ala Lys Gln Leu Thr Thr Thr
 535 540 545
 atc aac acc aac gca gag gcc ctc ttc aga ccc ggc cct ggc agc ttg 1855
 Ile Asn Thr Asn Ala Glu Ala Leu Phe Arg Pro Gly Pro Gly Ser Leu
 550 555 560
 cat ctg aag aat ggg ccg gag agc atc atg aac tca acg gag tac cca 1903
 His Leu Lys Asn Gly Pro Glu Ser Ile Met Asn Ser Thr Glu Tyr Pro
 565 570 575 580
 cac ggt ggc tcc cag gga cag ctg ctg cat cct ggt gac cac aag gcc 1951
 His Gly Gly Ser Gln Gly Gln Leu Leu His Pro Gly Asp His Lys Ala
 585 590 595
 cag gcc cac aac aag gca ctg ccc cca ggc ctg agc aag gag cag gcc 1999
 Gln Ala His Asn Lys Ala Leu Pro Pro Gly Leu Ser Lys Glu Gln Ala
 600 605 610
 cct gac tgt agc agc agt gat ggt tct gag agg agc tgg atg gat gac 2047
 Pro Asp Cys Ser Ser Ser Asp Gly Ser Glu Arg Ser Trp Met Asp Asp
 615 620 625
 tac gat tac gtc cac cta cag ggt aag gag gag ttt gag agg caa cag 2095
 Tyr Asp Tyr Val His Leu Gln Gly Lys Glu Glu Phe Glu Arg Gln Gln
 630 635 640
 aaa gag cta ttg gaa aaa gag aat atc atg aaa cag aac aag atg cag 2143
 Lys Glu Leu Leu Glu Lys Glu Asn Ile Met Lys Gln Asn Lys Met Gln
 645 650 655 660
 ctg gaa cat cat cag ctg agc cag ttc cag ctg ttg gaa caa gag att 2191
 Leu Glu His His Gln Leu Ser Gln Phe Gln Leu Leu Glu Gln Glu Ile

665 670 675
aca aag ccc gtg gag aat gac atc tgc aag tgg aag ccc tct cag agc 2239
Thr Lys Pro Val Glu Asn Asp Ile Ser Lys Trp Lys Pro Ser Gln Ser
680 685 690
cta ccc acc aca aac agt ggc gtg agt gct cag gat cgg cag ttg ctg 2287
Leu Pro Thr Thr Asn Ser Gly Val Ser Ala Gln Asp Arg Gln Leu Leu
695 700 705
tgc ttc tac tai gac caa tgt gag acc cat ttc att tcc ctt ctc aac 2335
Cys Phe Tyr Tyr Asp Gln Cys Glu Thr His Phe Ile Ser Leu Leu Asn
710 715 720
gcc att gac gca ctc ttc agt tgt gtc agc tca gcc cag ccc ccg cga 2383
Ala Ile Asp Ala Leu Phe Ser Cys Val Ser Ser Ala Gln Pro Pro Arg
725 730 735 740
atc ttc gtg gca cac agc aag ttt gtc atc ctc agt gca cac aaa ctg 2431
Ile Phe Val Ala His Ser Lys Phe Val Ile Leu Ser Ala His Lys Leu
745 750 755
gtg ttc att gga gac acg ctg aca cgg cag gtg act gcc cag gac att 2479
Val Phe Ile Gly Asp Thr Leu Thr Arg Gln Val Thr Ala Gln Asp Ile
760 765 770
cgc aac aaa gtc atg aac tcc agc aac cag ctc tgc gag cag ctc aag 2527
Arg Asn Lys Val Met Asn Ser Ser Asn Gln Leu Cys Glu Gln Leu Lys
775 780 785
act ata gtc atg gca acc aag atg gcc gcc ctc cat tac ccc agc acc 2575
Thr Ile Val Met Ala Thr Lys Met Ala Ala Leu His Tyr Pro Ser Thr
790 795 800
acg gcc ctg cag gaa atg gtg cac caa gtg aca gac ctt tct aga aat 2623
Thr Ala Leu Gln Glu Met Val His Gln Val Thr Asp Leu Ser Arg Asn

805	810	815	820	
gcc cag ctg ttc aag cgc tct ttg ctg gag atg gca acg ttc				2665
Ala Gln Leu Phe Lys Arg Ser Leu Leu Glu Met Ala Thr Phe				
	825	830		
tgagaagaaa	aaaaagagga	aggggacigc	gttaacgggt	actaaggaaa actggaaata 2725
ctgtctgggt	tttgtaaagt	ttatctatit	ttgtagataa	ttttatataa aaatgaaata 2785
ttttaacatt	ttatgggtca	gacaactttc	agaaattcag	ggagctggag agggaaatct 2845
ttttttcccc	cctgagtgtt	cttatgtata	cacagaagta	tctgagacat aaactgtaca 2905
gaaaacttgt	ccacgtcctt	ttgtatgccc	atgtattcat	gtttttgttt gtagatgttt 2965
gtctgatgca	tttcallaaa	aaaaaaacca	tgaattacga	agcaccttag taagcacctt 3025
ctaattgctgc	atTTTTTTTg	ttgttgttaa	aaacalccag	ctggttataa tattgtttctc 3085
cacgtccttg	tgatgattct	gagcctggca	ctgggaatct	gggaagcata gtttatttgc 3145
aaggtttcac	cttccaaatc	atgaggcata	gcatgactta	ticttgtttt gaaaactcct 3205
ttcaaaactg	accatcttaa	acacatgatg	gccaagtgcc	acaaagccct cttgcggaga 3265
catttacgaa	tatatatgtg	gatccaagtc	tcgatagtta	ggcgtlggag ggaagagaga 3325
ccagagagtt	tagaggccag	gaccacagtt	aggattgggt	tgtttcaata ctgagagaca 3385
gctacaataa	aaggagagca	attgcctccc	tggggctgtt	caatcttctg catttgtgag 3445
tggttcagtc	atgaggtttt	ccaaaagatg	tttttagagt	tgtaaaaacc atatttgcag 3505
caaagattta	caaaggcgta	tcagactatg	attgttcacc	aaaatagggg aatggtttga 3565
tccgccagtt	gcaagtagag	gcccttctga	ctcttaatat	tcactttggt gctactaccc 3625
ccattacctg	aggaactggc	caggiccttg	atcatggaac	tatagagcta ccagacatat 3685
cctgcctctt	aagggaattt	attgctatct	tgcaccttct	ttaaaactca aaaaacatat 3745
gcagacctga	cactcaagag	tggctagcta	cacagagtc	atctaatttt tgcaacttcc 3805
ccccccgaat	tc			3817

<210> 18

<211> 834

<212> PRT

<213> Homo sapiens

<400> 18

Met Lys Tyr Lys Asn Leu Met Ala Arg Ala Leu Tyr Asp Asn Val Pro

1 5 10 15

Glu Cys Ala Glu Glu Leu Ala Phe Arg Lys Gly Asp Ile Leu Thr Val

20 25 30

Ile Glu Gln Asn Thr Gly Gly Leu Glu Gly Trp Trp Leu Cys Ser Leu

35 40 45

His Gly Arg Gln Gly Ile Val Pro Gly Asn Arg Val Lys Leu Leu Ile

50 55 60

Gly Pro Met Gln Glu Thr Ala Ser Ser His Glu Gln Pro Ala Ser Gly

65 70 75 80

Leu Met Gln Gln Thr Phe Gly Gln Gln Lys Leu Tyr Gln Val Pro Asn

85 90 95

Pro Gln Ala Ala Pro Arg Asp Thr Ile Tyr Gln Val Pro Pro Ser Tyr

100 105 110

Gln Asn Gln Gly Ile Tyr Gln Val Pro Thr Gly His Gly Thr Gln Glu

115 120 125

Gln Glu Val Tyr Gln Val Pro Pro Ser Val Gln Arg Ser Ile Gly Gly

130 135 140

Thr Ser Gly Pro His Val Gly Lys Lys Val Ile Thr Pro Val Arg Thr

145 150 155 160

Gly His Gly Tyr Val Tyr Glu Tyr Pro Ser Arg Tyr Gln Lys Asp Val

165 170 175

Tyr Asp Ile Pro Pro Ser His Thr Thr Gln Gly Val Tyr Asp Ile Pro

180	185	190	
Pro Ser Ser Ala Lys Gly Pro Val Phe Ser Val Pro Val Gly Glu Ile			
195	200	205	
Lys Pro Gln Gly Val Tyr Asp Ile Pro Pro Thr Lys Gly Val Tyr Ala			
210	215	220	
Ile Pro Pro Ser Ala Cys Arg Asp Glu Ala Gly Leu Arg Glu Lys Asp			
225	230	235	240
Tyr Asp Phe Pro Pro Pro Met Arg Gln Ala Gly Arg Pro Asp Leu Arg			
245	250	255	
Pro Glu Gly Val Tyr Asp Ile Pro Pro Thr Cys Thr Lys Pro Ala Gly			
260	265	270	
Lys Asp Leu His Val Lys Tyr Asn Cys Asp Ile Pro Gly Ala Ala Glu			
275	280	285	
Pro Val Ala Arg Arg His Gln Ser Leu Ser Pro Asn His Pro Pro Pro			
290	295	300	
Gln Leu Gly Gln Ser Val Gly Ser Gln Asn Asp Ala Tyr Asp Val Pro			
305	310	315	320
Arg Gly Val Gln Phe Leu Glu Pro Pro Ala Glu Thr Ser Glu Lys Ala			
325	330	335	
Asn Pro Gln Glu Arg Asp Gly Val Tyr Asp Val Pro Leu His Asn Pro			
340	345	350	
Pro Asp Ala Lys Gly Ser Arg Asp Leu Val Asp Gly Ile Asn Arg Leu			
355	360	365	
Ser Phe Ser Ser Thr Gly Ser Thr Arg Ser Asn Met Ser Thr Ser Ser			
370	375	380	
Thr Ser Ser Lys Glu Ser Ser Leu Ser Ala Ser Pro Ala Gln Asp Lys			
385	390	395	400

Arg Leu Phe Leu Asp Pro Asp Thr Ala Ile Glu Arg Leu Gln Arg Leu			
405	410	415	
Gln Gln Ala Leu Glu Met Gly Val Ser Ser Leu Met Ala Leu Val Thr			
420	425	430	
Thr Asp Trp Arg Cys Tyr Gly Tyr Met Glu Arg His Ile Asn Glu Ile			
435	440	445	
Arg Thr Ala Val Asp Lys Val Glu Leu Phe Leu Lys Glu Tyr Leu His			
450	455	460	
Phe Val Lys Gly Ala Val Ala Asn Ala Ala Cys Leu Pro Glu Leu Ile			
465	470	475	480
Leu His Asn Lys Met Lys Arg Glu Leu Gln Arg Val Glu Asp Ser His			
485	490	495	
Gln Ile Leu Ser Gln Thr Ser His Asp Leu Asn Glu Cys Ser Trp Ser			
500	505	510	
Leu Asn Ile Leu Ala Ile Asn Lys Pro Gln Asn Lys Cys Asp Asp Leu			
515	520	525	
Asp Arg Phe Val Met Val Ala Lys Thr Val Pro Asp Asp Ala Lys Gln			
530	535	540	
Leu Thr Thr Thr Ile Asn Thr Asn Ala Glu Ala Leu Phe Arg Pro Gly			
545	550	555	560
Pro Gly Ser Leu His Leu Lys Asn Gly Pro Glu Ser Ile Met Asn Ser			
565	570	575	
Thr Glu Tyr Pro His Gly Gly Ser Gln Gly Gln Leu Leu His Pro Gly			
580	585	590	
Asp His Lys Ala Gln Ala His Asn Lys Ala Leu Pro Pro Gly Leu Ser			
595	600	605	

Lys Glu Gln Ala Pro Asp Cys Ser Ser Ser Asp Gly Ser Glu Arg Ser
610 615 620
Trp Met Asp Asp Tyr Asp Tyr Val His Leu Gln Gly Lys Glu Glu Phe
625 630 635 640
Glu Arg Gln Gln Lys Glu Leu Leu Glu Lys Glu Asn Ile Met Lys Gln
645 650 655
Asn Lys Met Gln Leu Glu His His Gln Leu Ser Gln Phe Gln Leu Leu
660 665 670
Glu Gln Glu Ile Thr Lys Pro Val Glu Asn Asp Ile Ser Lys Trp Lys
675 680 685
Pro Ser Gln Ser Leu Pro Thr Thr Asn Ser Gly Val Ser Ala Gln Asp
690 695 700
Arg Gln Leu Leu Cys Phe Tyr Tyr Asp Gln Cys Glu Thr His Phe Ile
705 710 715 720
Ser Leu Leu Asn Ala Ile Asp Ala Leu Phe Ser Cys Val Ser Ser Ala
725 730 735
Gln Pro Pro Arg Ile Phe Val Ala His Ser Lys Phe Val Ile Leu Ser
740 745 750
Ala His Lys Leu Val Phe Ile Gly Asp Thr Leu Thr Arg Gln Val Thr
755 760 765
Ala Gln Asp Ile Arg Asn Lys Val Met Asn Ser Ser Asn Gln Leu Cys
770 775 780
Glu Gln Leu Lys Thr Ile Val Met Ala Thr Lys Met Ala Ala Leu His
785 790 795 800
Tyr Pro Ser Thr Thr Ala Leu Gln Glu Met Val His Gln Val Thr Asp
805 810 815
Leu Ser Arg Asn Ala Gln Leu Phe Lys Arg Ser Leu Leu Glu Met Ala

820 825 830

Thr Phe

<210> 19

<211> 567

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (36).. (506)

<400> 19

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Met Leu Ala Gly Asn Glu

1 5

ttc cag gtg tcc ctg agc agc tcc atg tgc gtg tca gag ctg aag gcg 101

Phe Gln Val Ser Leu Ser Ser Ser Met Ser Val Ser Glu Leu Lys Ala

10 15 20

cag atc acc cag aac att ggc glg cac gcc ttc cag cag cgt ctg gct 149

Gln Ile Thr Gln Asn Ile Gly Val His Ala Phe Gln Gln Arg Leu Ala

25 30 35

gtc cac ccg agc ggt gtg gcg ctg cag gac agg gtc ccc ctt gcc agc 197

Val His Pro Ser Gly Val Ala Leu Gln Asp Arg Val Pro Leu Ala Ser

40 45 50

cag ggc ctg ggc cct ggc agc acg gtc ctg ctg gtg gtg gac aaa tgc 245

Gln Gly Leu Gly Pro Gly Ser Thr Val Leu Leu Val Val Asp Lys Cys

55 60 65 70

gac gaa cct ctg agc atc ctg gtg agg aat aac aag ggc cgc agc agc 293

Asp Glu Pro Leu Ser Ile Leu Val Arg Asn Asn Lys Gly Arg Ser Ser
 75 80 85
 acc tac gag gtg cgg ctg acg cag acc gtg gcc cac ctg aag cag caa 341
 Thr Tyr Glu Val Arg Leu Thr Gln Thr Val Ala His Leu Lys Gln Gln
 90 95 100
 gtg agc ggg ctg gag ggt gtg cag gac gac ctg ttc tgg ctg acc ttc 389
 Val Ser Gly Leu Glu Gly Val Gln Asp Asp Leu Phe Trp Leu Thr Phe
 105 110 115
 gag ggg aag ccc ctg gag gac cag ctc ccg ctg ggg gag tac ggc ctc 437
 Glu Gly Lys Pro Leu Glu Asp Gln Leu Pro Leu Gly Glu Tyr Gly Leu
 120 125 130
 aag ccc ctg agc acc glg ttc atg aat ctg cgc ctg cgg gga ggc ggc 485
 Lys Pro Leu Ser Thr Val Phe Met Asn Leu Arg Leu Arg Gly Gly Gly
 135 140 145 150
 aca gag cct ggc ggg cgg agc taagggcctc caccagcattc cgagcaggat 536
 Thr Glu Pro Gly Gly Arg Ser
 155
 caagggccgg aataaaggct gtgtgaagag a 567

<210> 20

<211> 157

<212> PRT

<213> Homo sapiens

<400> 20

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 Val Ser Glu Leu Lys Ala Gln Ile Thr Gln Asn Ile Gly Val His Ala

20 25 30
 Phe Gln Gln Arg Leu Ala Val His Pro Ser Gly Val Ala Leu Gln Asp
 35 40 45
 Arg Val Pro Leu Ala Ser Gln Gly Leu Gly Pro Gly Ser Thr Val Leu
 50 55 60
 Leu Val Val Asp Lys Cys Asp Glu Pro Leu Ser Ile Leu Val Arg Asn
 65 70 75 80
 Asn Lys Gly Arg Ser Ser Thr Tyr Glu Val Arg Leu Thr Gln Thr Val
 85 90 95
 Ala His Leu Lys Gln Gln Val Ser Gly Leu Glu Gly Val Gln Asp Asp
 100 105 110
 Leu Phe Trp Leu Thr Phe Glu Gly Lys Pro Leu Glu Asp Gln Leu Pro
 115 120 125
 Leu Gly Glu Tyr Gly Leu Lys Pro Leu Ser Thr Val Phe Met Asn Leu
 130 135 140
 Arg Leu Arg Gly Gly Gly Thr Glu Pro Gly Gly Arg Ser
 145 150 155

<210> 21

<211> 5095

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (14).. (2593)

<400> 21

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Met Gly Pro Trp Gly Trp Lys Leu Arg Trp Thr Val

1 5 10

gcc ttg ctc ctc gcc gcg gcg ggg act gca gtg ggc gac aga tgt gaa 97

Ala Leu Leu Leu Ala Ala Ala Gly Thr Ala Val Gly Asp Arg Cys Glu

15 20 25

aga aac gag ttc cag tgc caa gac ggg aaa tgc atc tcc tac aag tgg 145

Arg Asn Glu Phe Gln Cys Gln Asp Gly Lys Cys Ile Ser Tyr Lys Trp

30 35 40

gtc tgc gat ggc agc gct gag tgc cag gat ggc tct gat gag tcc cag 193

Val Cys Asp Gly Ser Ala Glu Cys Gln Asp Gly Ser Asp Glu Ser Gln

45 50 55 60

gag acg tgc ttg tct gtc acc tgc aaa tcc ggg gac ttc agc tgt ggg 241

Glu Thr Cys Leu Ser Val Thr Cys Lys Ser Gly Asp Phe Ser Cys Gly

65 70 75

ggc cgt gtc aac cgc tgc att cct cag ttc tgg agg tgc gat ggc caa 289

Gly Arg Val Asn Arg Cys Ile Pro Gln Phe Trp Arg Cys Asp Gly Gln

80 85 90

gtg gac tgc gac aac ggc tca gac gag caa ggc tgt ccc ccc aag acg 337

Val Asp Cys Asp Asn Gly Ser Asp Glu Gln Gly Cys Pro Pro Lys Thr

95 100 105

tgc tcc cag gac gag ttt cgc tgc cac gat ggg aag tgc atc tct cgg 385

Cys Ser Gln Asp Glu Phe Arg Cys His Asp Gly Lys Cys Ile Ser Arg

110 115 120

cag ttc gtc tgt gac tca gac cgg gac tgc ttg gac ggc tca gac gag 433

Gln Phe Val Cys Asp Ser Asp Arg Asp Cys Leu Asp Gly Ser Asp Glu

125 130 135 140

gcc tcc tgc ccg gtc ctc acc tgt ggt ccc gcc agc ttc cag tgc aac 481
 Ala Ser Cys Pro Val Leu Thr Cys Gly Pro Ala Ser Phe Gln Cys Asn
 145 150 155
 agc tcc acc tgc atc ccc cag ctc tgg gcc tgc gac aac gac ccc gac 529
 Ser Ser Thr Cys Ile Pro Gln Leu Trp Ala Cys Asp Asn Asp Pro Asp
 160 165 170
 tgc gaa gat ggc tgc gat gag tgg ccg cag cgc tgt agg ggt ctt tac 577
 Cys Glu Asp Gly Ser Asp Glu Trp Pro Gln Arg Cys Arg Gly Leu Tyr
 175 180 185
 gtg ttc caa ggg gac agt agc ccc tgc tgc gcc ttc gag ttc cac tgc 625
 Val Phe Gln Gly Asp Ser Ser Pro Cys Ser Ala Phe Glu Phe His Cys
 190 195 200
 cta agt ggc gag tgc atc cac tcc agc tgg cgc tgt gat ggt ggc ccc 673
 Leu Ser Gly Glu Cys Ile His Ser Ser Trp Arg Cys Asp Gly Gly Pro
 205 210 215 220
 gac tgc aag gac aaa tct gac gag gaa aac tgc gct gtg gcc acc tgt 721
 Asp Cys Lys Asp Lys Ser Asp Glu Glu Asn Cys Ala Val Ala Thr Cys
 225 230 235
 cgc cct gac gaa ttc cag tgc tct gat gga aac tgc atc cat ggc agc 769
 Arg Pro Asp Glu Phe Gln Cys Ser Asp Gly Asn Cys Ile His Gly Ser
 240 245 250
 cgg cag tgt gac cgg gaa tat gac tgc aag gac atg agc gat gaa gtt 817
 Arg Gln Cys Asp Arg Glu Tyr Asp Cys Lys Asp Met Ser Asp Glu Val
 255 260 265
 ggc tgc gtt aat gtg aca ctc tgc gag gga ccc aac aag ttc aag tgt 865
 Gly Cys Val Asn Val Thr Leu Cys Glu Gly Pro Asn Lys Phe Lys Cys
 270 275 280

cac agc ggc gaa tgc atc acc ctg gac aaa gtc tgc aac atg gct aga 913
 His Ser Gly Glu Cys Ile Thr Leu Asp Lys Val Cys Asn Met Ala Arg
 285 290 295 300
 gac tgc cgg gac tgg tca gat gaa ccc atc aaa gag tgc ggg acc aac 961
 Asp Cys Arg Asp Trp Ser Asp Glu Pro Ile Lys Glu Cys Gly Thr Asn
 305 310 315
 gaa tgc ttg gac aac aac ggc ggc tgt tcc cac gtc tgc aat gac ctt 1009
 Glu Cys Leu Asp Asn Asn Gly Gly Cys Ser His Val Cys Asn Asp Leu
 320 325 330
 aag atc ggc tac gag tgc ctg tgc ccc gac ggc ttc cag ctg gtg gcc 1057
 Lys Ile Gly Tyr Glu Cys Leu Cys Pro Asp Gly Phe Gln Leu Val Ala
 335 340 345
 cag cga aga tgc gaa gat atc gat gag tgt cag gat ccc gac acc tgc 1105
 Gln Arg Arg Cys Glu Asp Ile Asp Glu Cys Gln Asp Pro Asp Thr Cys
 350 355 360
 agc cag ctc tgc gtg aac ctg gag ggt ggc tac aag tgc cag tgt gag 1153
 Ser Gln Leu Cys Val Asn Leu Glu Gly Gly Tyr Lys Cys Gln Cys Glu
 365 370 375 380
 gaa ggc ttc cag ctg gac ccc cac acg aag gcc tgc aag gct gtg ggc 1201
 Glu Gly Phe Gln Leu Asp Pro His Thr Lys Ala Cys Lys Ala Val Gly
 385 390 395
 tcc atc gcc tac ctc ttc ttc acc aac cgg cac gag gtc agg aag atg 1249
 Ser Ile Ala Tyr Leu Phe Phe Thr Asn Arg His Glu Val Arg Lys Met
 400 405 410
 acg ctg gac cgg agc gag tac acc agc ctc atc ccc aac ctg agg aac 1297
 Thr Leu Asp Arg Ser Glu Tyr Thr Ser Leu Ile Pro Asn Leu Arg Asn

415 420 425
gtg gtc gct ctg gac acg gag gtg gcc agc aat aga atc tac tgg tct 1345
Val Val Ala Leu Asp Thr Glu Val Ala Ser Asn Arg Ile Tyr Trp Ser
430 435 440
gac ctg tcc cag aga atg atc tgc agc acc cag ctt gac aga gcc cac 1393
Asp Leu Ser Gln Arg Met Ile Cys Ser Thr Gln Leu Asp Arg Ala His
445 450 455 460
ggc gtc tct tcc tat gac acc gtc atc agc agg gac atc cag gcc ccc 1441
Gly Val Ser Ser Tyr Asp Thr Val Ile Ser Arg Asp Ile Gln Ala Pro
465 470 475
gac ggg ctg gct gtg gac tgg atc cac agc aac atc tac tgg acc gac 1489
Asp Gly Leu Ala Val Asp Trp Ile His Ser Asn Ile Tyr Trp Thr Asp
480 485 490
tct gtc ctg ggc act gtc tct gtt gcg gat acc aag ggc gtg aag agg 1537
Ser Val Leu Gly Thr Val Ser Val Ala Asp Thr Lys Gly Val Lys Arg
495 500 505
aaa acg tta ttc agg gag aac ggc tcc aag cca agg gcc atc gtg gtg 1585
Lys Thr Leu Phe Arg Glu Asn Gly Ser Lys Pro Arg Ala Ile Val Val
510 515 520
gat cct gtt cat ggc ttc atg tac tgg act gac tgg gga act ccc gcc 1633
Asp Pro Val His Gly Phe Met Tyr Trp Thr Asp Trp Gly Thr Pro Ala
525 530 535 540
aag atc aag aaa ggg ggc ctg aat ggt gtg gac atc tac tcg ctg gtg 1681
Lys Ile Lys Lys Gly Gly Leu Asn Gly Val Asp Ile Tyr Ser Leu Val
545 550 555
act gaa aac att cag tgg ccc aat ggc atc acc cta gat ctc ctc agt 1729
Thr Glu Asn Ile Gln Trp Pro Asn Gly Ile Thr Leu Asp Leu Leu Ser

560	565	570	
ggc cgc ctc tac tgg gtt gac tcc aaa ctt cac tcc atc tca agc atc	1777		
Gly Arg Leu Tyr Trp Val Asp Ser Lys Leu His Ser Ile Ser Ser Ile			
575	580	585	
gat gtc aat ggg ggc aac cgg aag acc atc ttg gag gat gaa aag agg	1825		
Asp Val Asn Gly Gly Asn Arg Lys Thr Ile Leu Glu Asp Glu Lys Arg			
590	595	600	
ctg gcc cac ccc ttc tcc ttg gcc gtc ttt gag gac aaa gta ttt tgg	1873		
Leu Ala His Pro Phe Ser Leu Ala Val Phe Glu Asp Lys Val Phe Trp			
605	610	615	620
aca gat atc atc aac gaa gcc att ttc agt gcc aac cgc ctc aca ggt	1921		
Thr Asp Ile Ile Asn Glu Ala Ile Phe Ser Ala Asn Arg Leu Thr Gly			
625	630	635	
tcc gat gtc aac ttg ttg gct gaa aac cta ctg tcc cca gag gat atg	1969		
Ser Asp Val Asn Leu Leu Ala Glu Asn Leu Leu Ser Pro Glu Asp Met			
640	645	650	
gtc ctc ttc cac aac ctc acc cag cca aga gga gtg aac tgg tgt gag	2017		
Val Leu Phe His Asn Leu Thr Gln Pro Arg Gly Val Asn Trp Cys Glu			
655	660	665	
agg acc acc ctg agc aat ggc ggc tgc cag tat ctg tgc ctc cct gcc	2065		
Arg Thr Thr Leu Ser Asn Gly Gly Cys Gln Tyr Leu Cys Leu Pro Ala			
670	675	680	
ccg cag atc aac ccc cac tcg ccc aag ttt acc tgc gcc tgc ccg gac	2113		
Pro Gln Ile Asn Pro His Ser Pro Lys Phe Thr Cys Ala Cys Pro Asp			
685	690	695	700
ggc atg ctg ctg gcc agg gac atg agg agc tgc ctc aca gag gct gag	2161		

Gly Met Leu Leu Ala Arg Asp Met Arg Ser Cys Leu Thr Glu Ala Glu
 705 710 715
 gct gca glg gcc acc cag gag aca tcc acc glc agg cta aag gtc agc 2209
 Ala Ala Val Ala Thr Gln Glu Thr Ser Thr Val Arg Leu Lys Val Ser
 720 725 730
 tcc aca gcc gta agg aca cag cac aca acc acc cgg cct gtt ccc gac 2257
 Ser Thr Ala Val Arg Thr Gln His Thr Thr Thr Arg Pro Val Pro Asp
 735 740 745
 acc tcc cgg ctg cct ggg gcc acc cct ggg ctc acc acg gtg gag ata 2305
 Thr Ser Arg Leu Pro Gly Ala Thr Pro Gly Leu Thr Thr Val Glu Ile
 750 755 760
 gtg aca atg tct cac caa gct ctg ggc gac gtt gct ggc aga gga aat 2353
 Val Thr Met Ser His Gln Ala Leu Gly Asp Val Ala Gly Arg Gly Asn
 765 770 775 780
 gag aag aag ccc agt agc gtg agg gct ctg tcc att gtc ctc ccc atc 2401
 Glu Lys Lys Pro Ser Ser Val Arg Ala Leu Ser Ile Val Leu Pro Ile
 785 790 795
 gtg ctc ctc gtc ttc ctt tgc ctg ggg gtc ttc ctt cta tgg aag aac 2449
 Val Leu Leu Val Phe Leu Cys Leu Gly Val Phe Leu Leu Trp Lys Asn
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 Trp Arg Leu Lys Asn Ile Asn Ser Ile Asn Phe Asp Asn Pro Val Tyr
 815 820 825
 cag aag acc aca gag gat gag gtc cac att tgc cac aac cag gac ggc 2545
 Gln Lys Thr Thr Glu Asp Glu Val His Ile Cys His Asn Gln Asp Gly
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Tyr Ser Tyr Pro Ser Arg Gln Met Val Ser Leu Glu Asp Asp Val Ala

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<211> 860

<212> PRT

<213> Homo sapiens

<400> 22

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 Ser Val Thr Cys Lys Ser Gly Asp Phe Ser Cys Gly Gly Arg Val Asn
 65 70 75 80
 Arg Cys Ile Pro Gln Phe Trp Arg Cys Asp Gly Gln Val Asp Cys Asp
 85 90 95
 Asn Gly Ser Asp Glu Gln Gly Cys Pro Pro Lys Thr Cys Ser Gln Asp
 100 105 110
 Glu Phe Arg Cys His Asp Gly Lys Cys Ile Ser Arg Gln Phe Val Cys
 115 120 125
 Asp Ser Asp Arg Asp Cys Leu Asp Gly Ser Asp Glu Ala Ser Cys Pro
 130 135 140
 Val Leu Thr Cys Gly Pro Ala Ser Phe Gln Cys Asn Ser Ser Thr Cys
 145 150 155 160
 Ile Pro Gln Leu Trp Ala Cys Asp Asn Asp Pro Asp Cys Glu Asp Gly
 165 170 175
 Ser Asp Glu Trp Pro Gln Arg Cys Arg Gly Leu Tyr Val Phe Gln Gly
 180 185 190
 Asp Ser Ser Pro Cys Ser Ala Phe Glu Phe His Cys Leu Ser Gly Glu
 195 200 205
 Cys Ile His Ser Ser Trp Arg Cys Asp Gly Gly Pro Asp Cys Lys Asp
 210 215 220
 Lys Ser Asp Glu Glu Asn Cys Ala Val Ala Thr Cys Arg Pro Asp Glu
 225 230 235 240

Phe Gln Cys Ser Asp Gly Asn Cys Ile His Gly Ser Arg Gln Cys Asp
 245 250 255
 Arg Glu Tyr Asp Cys Lys Asp Met Ser Asp Glu Val Gly Cys Val Asn
 260 265 270
 Val Thr Leu Cys Glu Gly Pro Asn Lys Phe Lys Cys His Ser Gly Glu
 275 280 285
 Cys Ile Thr Leu Asp Lys Val Cys Asn Met Ala Arg Asp Cys Arg Asp
 290 295 300
 Trp Ser Asp Glu Pro Ile Lys Glu Cys Gly Thr Asn Glu Cys Leu Asp
 305 310 315 320
 Asn Asn Gly Gly Cys Ser His Val Cys Asn Asp Leu Lys Ile Gly Tyr
 325 330 335
 Glu Cys Leu Cys Pro Asp Gly Phe Gln Leu Val Ala Gln Arg Arg Cys
 340 345 350
 Glu Asp Ile Asp Glu Cys Gln Asp Pro Asp Thr Cys Ser Gln Leu Cys
 355 360 365
 Val Asn Leu Glu Gly Gly Tyr Lys Cys Gln Cys Glu Glu Gly Phe Gln
 370 375 380
 Leu Asp Pro His Thr Lys Ala Cys Lys Ala Val Gly Ser Ile Ala Tyr
 385 390 395 400
 Leu Phe Phe Thr Asn Arg His Glu Val Arg Lys Met Thr Leu Asp Arg
 405 410 415
 Ser Glu Tyr Thr Ser Leu Ile Pro Asn Leu Arg Asn Val Val Ala Leu
 420 425 430
 Asp Thr Glu Val Ala Ser Asn Arg Ile Tyr Trp Ser Asp Leu Ser Gln
 435 440 445

Arg Met Ile Cys Ser Thr Gln Leu Asp Arg Ala His Gly Val Ser Ser
450 455 460

Tyr Asp Thr Val Ile Ser Arg Asp Ile Gln Ala Pro Asp Gly Leu Ala
465 470 475 480

Val Asp Trp Ile His Ser Asn Ile Tyr Trp Thr Asp Ser Val Leu Gly
485 490 495

Thr Val Ser Val Ala Asp Thr Lys Gly Val Lys Arg Lys Thr Leu Phe
500 505 510

Arg Glu Asn Gly Ser Lys Pro Arg Ala Ile Val Val Asp Pro Val His
515 520 525

Gly Phe Met Tyr Trp Thr Asp Trp Gly Thr Pro Ala Lys Ile Lys Lys
530 535 540

Gly Gly Leu Asn Gly Val Asp Ile Tyr Ser Leu Val Thr Glu Asn Ile
545 550 555 560

Gln Trp Pro Asn Gly Ile Thr Leu Asp Leu Leu Ser Gly Arg Leu Tyr
565 570 575

Trp Val Asp Ser Lys Leu His Ser Ile Ser Ser Ile Asp Val Asn Gly
580 585 590

Gly Asn Arg Lys Thr Ile Leu Glu Asp Glu Lys Arg Leu Ala His Pro
595 600 605

Phe Ser Leu Ala Val Phe Glu Asp Lys Val Phe Trp Thr Asp Ile Ile
610 615 620

Asn Glu Ala Ile Phe Ser Ala Asn Arg Leu Thr Gly Ser Asp Val Asn
625 630 635 640

Leu Leu Ala Glu Asn Leu Leu Ser Pro Glu Asp Met Val Leu Phe His
645 650 655

Asn Leu Thr Gln Pro Arg Gly Val Asn Trp Cys Glu Arg Thr Thr Leu

660 665 670
 Ser Asn Gly Gly Cys Gln Tyr Leu Cys Leu Pro Ala Pro Gln Ile Asn
 675 680 685
 Pro His Ser Pro Lys Phe Thr Cys Ala Cys Pro Asp Gly Met Leu Leu
 690 695 700
 Ala Arg Asp Met Arg Ser Cys Leu Thr Glu Ala Glu Ala Ala Val Ala
 705 710 715 720
 Thr Gln Glu Thr Ser Thr Val Arg Leu Lys Val Ser Ser Thr Ala Val
 725 730 735
 Arg Thr Gln His Thr Thr Thr Arg Pro Val Pro Asp Thr Ser Arg Leu
 740 745 750
 Pro Gly Ala Thr Pro Gly Leu Thr Thr Val Glu Ile Val Thr Met Ser
 755 760 765
 His Gln Ala Leu Gly Asp Val Ala Gly Arg Gly Asn Glu Lys Lys Pro
 770 775 780
 Ser Ser Val Arg Ala Leu Ser Ile Val Leu Pro Ile Val Leu Leu Val
 785 790 795 800
 Phe Leu Cys Leu Gly Val Phe Leu Leu Trp Lys Asn Trp Arg Leu Lys
 805 810 815
 Asn Ile Asn Ser Ile Asn Phe Asp Asn Pro Val Tyr Gln Lys Thr Thr
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<212> DNA

<213> Homo sapiens

<220>

<221> CDS

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<400> 23

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Leu Leu Leu Ser Ile Ile Val Leu His Val Ala Val Leu Val Leu Leu

5

10

15

ttc gtc tcc acg atc gtc agc caa tgg atc gtg ggc aat gga cac gca 154

Phe Val Ser Thr Ile Val Ser Gln Trp Ile Val Gly Asn Gly His Ala

20

25

30

35

act gat ctc tgg cag aac tgt agc acc tct tcc tca gga aat gtc cac 202

Thr Asp Leu Trp Gln Asn Cys Ser Thr Ser Ser Ser Gly Asn Val His

40

45

50

cac tgt ttc tca tca tca cca aac gaa tgg ctg cag tct gtc cag gcc 250

His Cys Phe Ser Ser Ser Pro Asn Glu Trp Leu Gln Ser Val Gln Ala

55

60

65

acc atg atc ctg tcg atc atc ttc agc att ctg tct ctg ttc ctg ttc 298

Thr Met Ile Leu Ser Ile Ile Phe Ser Ile Leu Ser Leu Phe Leu Phe

70

75

80

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Phe Cys Gln Leu Phe Thr Leu Thr Lys Gly Gly Arg Phe Tyr Ile Thr
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 gga atc ttc caa att ctt gct ggt ctg tgc glg atg agt gct gcg gcc 394
 Gly Ile Phe Gln Ile Leu Ala Gly Leu Cys Val Met Ser Ala Ala Ala
 100 105 110 115
 atc tac acg gtg agg cac ccg gag tgg cat ctc acc tcg gat tac tcc 442
 Ile Tyr Thr Val Arg His Pro Glu Trp His Leu Thr Ser Asp Tyr Ser
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<212> PRT

<213> Homo sapiens

<400> 24

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Gly His Ala Thr Asp Leu Trp Gln Asn Cys Ser Thr Ser Ser Ser Gly

35 40 45

Asn Val His His Cys Phe Ser Ser Ser Pro Asn Glu Trp Leu Gln Ser

50 55 60

Val Gln Ala Thr Met Ile Leu Ser Ile Ile Phe Ser Ile Leu Ser Leu

65 70 75 80

Phe Leu Phe Phe Cys Gln Leu Phe Thr Leu Thr Lys Gly Gly Arg Phe

85 90 95

Tyr Ile Thr Gly Ile Phe Gln Ile Leu Ala Gly Leu Cys Val Met Ser

100 105 110

Ala Ala Ala Ile Tyr Thr Val Arg His Pro Glu Trp His Leu Thr Ser

115 120 125
 Asp Tyr Ser Tyr Gly Phe Ala Tyr Ile Leu Ala Trp Val Ala Phe Pro
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<210> 25

<211> 3116

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (36).. (2717)

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Arg Met Gly Arg Val Pro Leu Ala Trp Cys Leu Ala Leu Cys Gly Trp

10

15

20

gcg tgc atg gcc ccc agg ggc acg cag gct gaa gaa agt ccc ttc gtg 149

Ala Cys Met Ala Pro Arg Gly Thr Gln Ala Glu Glu Ser Pro Phe Val

25

30

35

ggc aac cca ggg aat atc aca ggt gcc cgg gga ctc acg ggc acc ctt 197

Gly Asn Pro Gly Asn Ile Thr Gly Ala Arg Gly Leu Thr Gly Thr Leu

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45

50

cgg tgt cag ctc cag gtt cag gga gag ccc ccc gag gta cat tgg ctt 245

Arg Cys Gln Leu Gln Val Gln Gly Glu Pro Pro Glu Val His Trp Leu
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 cgg gat gga cag atc ctg gag ctc gcg gac agc acc cag acc cag gtg 293
 Arg Asp Gly Gln Ile Leu Glu Leu Ala Asp Ser Thr Gln Thr Gln Val
 75 80 85
 ccc ctg ggt gag gat gaa cag gat gac tgg ata gtg gtc agc cag ctc 341
 Pro Leu Gly Glu Asp Glu Gln Asp Asp Trp Ile Val Val Ser Gln Leu
 90 95 100
 aga atc acc tcc ctg cag ctt tcc gac acg gga cag tac cag tgt ttg 389
 Arg Ile Thr Ser Leu Gln Leu Ser Asp Thr Gly Gln Tyr Gln Cys Leu
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 gtg ttt ctg gga cat cag acc ttc gtg tcc cag cct ggc tat gtt ggg 437
 Val Phe Leu Gly His Gln Thr Phe Val Ser Gln Pro Gly Tyr Val Gly
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 Leu Glu Gly Leu Pro Tyr Phe Leu Glu Glu Pro Glu Asp Arg Thr Val
 135 140 145 150
 gcc gcc aac acc ccc ttc aac ctg agc tgc caa gct cag gga ccc cca 533
 Ala Ala Asn Thr Pro Phe Asn Leu Ser Cys Gln Ala Gln Gly Pro Pro
 155 160 165
 gag ccc gtg gac cta ctc tgg ctc cag gat gct gtc ccc ctg gcc acg 581
 Glu Pro Val Asp Leu Leu Trp Leu Gln Asp Ala Val Pro Leu Ala Thr
 170 175 180
 gct cca ggt cac ggc ccc cag cgc agc ctg cat gtt cca ggg ctg aac 629
 Ala Pro Gly His Gly Pro Gln Arg Ser Leu His Val Pro Gly Leu Asn
 185 190 195

aag aca tcc tct ttc tcc tgc gaa gcc cat aac gcc aag ggg gtc acc 677
Lys Thr Ser Ser Phe Ser Cys Glu Ala His Asn Ala Lys Gly Val Thr
200 205 210
aca tcc cgc aca gcc acc atc aca gtg ctc ccc cag cag ccc cgt aac 725
Thr Ser Arg Thr Ala Thr Ile Thr Val Leu Pro Gln Gln Pro Arg Asn
215 220 225 230
ctc cac ctg gtc tcc cgc caa ccc acg gag ctg gag gtg gct tgg act 773
Leu His Leu Val Ser Arg Gln Pro Thr Glu Leu Glu Val Ala Trp Thr
235 240 245
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Pro Gly Leu Ser Gly Ile Tyr Pro Leu Thr His Cys Thr Leu Gln Ala
250 255 260
gtg ctg tca gac gat ggg atg ggc atc cag gcg gga gaa cca gac ccc 869
Val Leu Ser Asp Asp Gly Met Gly Ile Gln Ala Gly Glu Pro Asp Pro
265 270 275
cca gag gag ccc ctc acc tcg caa gca tcc gtg ccc ccc cat cag ctt 917
Pro Glu Glu Pro Leu Thr Ser Gln Ala Ser Val Pro Pro His Gln Leu
280 285 290
cgg cta ggc agc ctc cat cct cac ccc cct tat cac atc cgc gtg gca 965
Arg Leu Gly Ser Leu His Pro His Pro Pro Tyr His Ile Arg Val Ala
295 300 305 310
tgc acc agc agc cag ggc ccc tca tcc tgg acc cac tgg ctt cct gtg 1013
Cys Thr Ser Ser Gln Gly Pro Ser Ser Trp Thr His Trp Leu Pro Val
315 320 325
gag acg ccg gag gga gtg ccc ctg ggc ccc cct gag aac att agt gct 1061
Glu Thr Pro Glu Gly Val Pro Leu Gly Pro Pro Glu Asn Ile Ser Ala
330 335 340

acg cgg aat ggg agc cag gcc ttc gtg cat tgg caa gag ccc cgg gcg 1109
 Thr Arg Asn Gly Ser Gln Ala Phe Val His Trp Gln Glu Pro Arg Ala
 345 350 355
 ccc ctg cag ggt acc ctg tta ggg tac cgg ctg gcg tat caa ggc cag 1157
 Pro Leu Gln Gly Thr Leu Leu Gly Tyr Arg Leu Ala Tyr Gln Gly Gln
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 gac acc cca gag gtg cta atg gac ata ggg cta agg caa gag gtg acc 1205
 Asp Thr Pro Glu Val Leu Met Asp Ile Gly Leu Arg Gln Glu Val Thr
 375 380 385 390
 ctg gag ctg cag ggg gac ggg tct gtg tcc aat ctg aca gtg tgt gtg 1253
 Leu Glu Leu Gln Gly Asp Gly Ser Val Ser Asn Leu Thr Val Cys Val
 395 400 405
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 Ala Ala Tyr Thr Ala Ala Gly Asp Gly Pro Trp Ser Leu Pro Val Pro
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 ctg gag gcc tgg cgc cca ggg gaa gca cag cca gtc cac cag ctg gtg 1349
 Leu Glu Ala Trp Arg Pro Gly Glu Ala Gln Pro Val His Gln Leu Val
 425 430 435
 aag gaa cct tca act cct gcc ttc tgg tgg ccc tgg tgg tat gla ctg 1397
 Lys Glu Pro Ser Thr Pro Ala Phe Ser Trp Pro Trp Trp Tyr Val Leu
 440 445 450
 cta gga gca gtc gtg gcc gct gcc tgt gtc ctc atc ttg gct ctc ttc 1445
 Leu Gly Ala Val Val Ala Ala Ala Cys Val Leu Ile Leu Ala Leu Phe
 455 460 465 470
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 Leu Val His Arg Arg Lys Lys Glu Thr Arg Tyr Gly Glu Val Phe Glu

475	480	485	
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Pro Thr Val Glu Arg Gly Glu Leu Val Val Arg Tyr Arg Val Arg Lys			
490	495	500	
tcc tac agt cgt cgg acc act gaa gct acc ttg aac agc ctg ggc atc			1589
Ser Tyr Ser Arg Arg Thr Thr Glu Ala Thr Leu Asn Ser Leu Gly Ile			
505	510	515	
agt gaa gag ctg aag gag aag ctg cgg gat gtg atg gtg gac cgg cac			1637
Ser Glu Glu Leu Lys Glu Lys Leu Arg Asp Val Met Val Asp Arg His			
520	525	530	
aag gtg gcc ctg ggg aag act ctg gga gag gga gag ttt gga gct gtg			1685
Lys Val Ala Leu Gly Lys Thr Leu Gly Glu Gly Glu Phe Gly Ala Val			
535	540	545	550
atg gaa ggc cag ctc aac cag gac gac tcc atc ctc aag gtg gct gtg			1733
Met Glu Gly Gln Leu Asn Gln Asp Asp Ser Ile Leu Lys Val Ala Val			
555	560	565	
aag acg atg aag att gcc atc tgc acg agg tca gag ctg gag gat ttc			1781
Lys Thr Met Lys Ile Ala Ile Cys Thr Arg Ser Glu Leu Glu Asp Phe			
570	575	580	
ctg agt gaa gcg gtc tgc atg aag gaa ttt gac cat ccc aac gtc atg			1829
Leu Ser Glu Ala Val Cys Met Lys Glu Phe Asp His Pro Asn Val Met			
585	590	595	
agg ctc atc ggt gtc tgt ttc cag ggt tct gaa cga gag agc ttc cca			1877
Arg Leu Ile Gly Val Cys Phe Gln Gly Ser Glu Arg Glu Ser Phe Pro			
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gca cct gtg gtc atc tta cct ttc atg aaa cat gga gac cta cac agc			1925
Ala Pro Val Val Ile Leu Pro Phe Met Lys His Gly Asp Leu His Ser			

615	620	625	630	
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Phe Leu Leu Tyr Ser Arg Leu Gly Gly Gln Pro Val Tyr Leu Pro Thr				
	635	640	645	
cag atg cta gtg aag ttc atg gca gac atc gcc agt ggc atg gag tat				2021
Gln Met Leu Val Lys Phe Met Ala Asp Ile Ala Ser Gly Met Glu Tyr				
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ctg agt acc aag aga ttc ata cac cgg gac ctg gcg gcc agg aac tgc				2069
Leu Ser Thr Lys Arg Phe Ile His Arg Asp Leu Ala Ala Arg Asn Cys				
	665	670	675	
atg ctg aat gag aac atg tcc gtg tgt gtg gcg gac ttc ggg ctc tcc				2117
Met Leu Asn Glu Asn Met Ser Val Cys Val Ala Asp Phe Gly Leu Ser				
	680	685	690	
aag aag atc tac aat ggg gac tac tac cgc cag gga cgt atc gcc aag				2165
Lys Lys Ile Tyr Asn Gly Asp Tyr Tyr Arg Gln Gly Arg Ile Ala Lys				
695	700	705	710	
atg cca gtc aag tgg att gcc att gag agt cta gct gac cgt gtc tac				2213
Met Pro Val Lys Trp Ile Ala Ile Glu Ser Leu Ala Asp Arg Val Tyr				
	715	720	725	
acc agc aag agc gat gtg tgg tcc ttc ggg gtg aca atg tgg gag att				2261
Thr Ser Lys Ser Asp Val Trp Ser Phe Gly Val Thr Met Trp Glu Ile				
	730	735	740	
gcc aca aga ggc caa acc cca tat ccg ggc gtg gag aac agc gag att				2309
Ala Thr Arg Gly Gln Thr Pro Tyr Pro Gly Val Glu Asn Ser Glu Ile				
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tat gac tat ctg cgc cag gga aat cgc ctg aag cag cct gcg gac tgt				2357

Tyr Asp Tyr Leu Arg Gln Gly Asn Arg Leu Lys Gln Pro Ala Asp Cys
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 ctg gat gga ctg tat gcc ttg atg tcg cgg tgc tgg gag cta aat ccc 2405
 Leu Asp Gly Leu Tyr Ala Leu Met Ser Arg Cys Trp Glu Leu Asn Pro
 775 780 785 790
 cag gac cgg cca agt ttt aca gag ctg cgg gaa gat ttg gag aac aca 2453
 Gln Asp Arg Pro Ser Phe Thr Glu Leu Arg Glu Asp Leu Glu Asn Thr
 795 800 805
 ctg aag gcc ttg cct cct gcc cag gag cct gac gaa atc ctc tat gtc 2501
 Leu Lys Ala Leu Pro Pro Ala Gln Glu Pro Asp Glu Ile Leu Tyr Val
 810 815 820
 aac atg gat gag ggt gga ggt tat cct gaa ccc cct gga gct gca gga 2549
 Asn Met Asp Glu Gly Gly Gly Tyr Pro Glu Pro Pro Gly Ala Ala Gly
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 gga gct gac ccc cca acc cag cca gac cct aag gat tcc tgt agc tgc 2597
 Gly Ala Asp Pro Pro Thr Gln Pro Asp Pro Lys Asp Ser Cys Ser Cys
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 Leu Thr Ala Ala Glu Val His Pro Ala Gly Arg Tyr Val Leu Cys Pro
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 Ser Thr Thr Pro Ser Pro Ala Gln Pro Ala Asp Arg Gly Ser Pro Ala
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35 40 45

Gly Leu Thr Gly Thr Leu Arg Cys Gln Leu Gln Val Gln Gly Glu Pro

50 55 60

Pro Glu Val His Trp Leu Arg Asp Gly Gln Ile Leu Glu Leu Ala Asp

65 70 75 80

Ser Thr Gln Thr Gln Val Pro Leu Gly Glu Asp Glu Gln Asp Asp Trp

85 90 95

Ile Val Val Ser Gln Leu Arg Ile Thr Ser Leu Gln Leu Ser Asp Thr

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Gly Gln Tyr Gln Cys Leu Val Phe Leu Gly His Gln Thr Phe Val Ser

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 Gln Pro Gly Tyr Val Gly Leu Glu Gly Leu Pro Tyr Phe Leu Glu Glu
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 145 150 155 160
 Gln Ala Gln Gly Pro Pro Glu Pro Val Asp Leu Leu Trp Leu Gln Asp
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 Ala Val Pro Leu Ala Thr Ala Pro Gly His Gly Pro Gln Arg Ser Leu
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 His Val Pro Gly Leu Asn Lys Thr Ser Ser Phe Ser Cys Glu Ala His
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 Asn Ala Lys Gly Val Thr Thr Ser Arg Thr Ala Thr Ile Thr Val Leu
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 Pro Gln Gln Pro Arg Asn Leu His Leu Val Ser Arg Gln Pro Thr Glu
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 245 250 255
 His Cys Thr Leu Gln Ala Val Leu Ser Asp Asp Gly Met Gly Ile Gln
 260 265 270
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 Val Pro Pro His Gln Leu Arg Leu Gly Ser Leu His Pro His Pro Pro
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 Thr His Trp Leu Pro Val Glu Thr Pro Glu Gly Val Pro Leu Gly Pro

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Asn Leu Thr Val Cys Val Ala Ala Tyr Thr Ala Ala Gly Asp Gly Pro
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Pro Val His Gln Leu Val Lys Glu Pro Ser Thr Pro Ala Phe Ser Trp
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485 490 495
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 Ser Glu Leu Glu Asp Phe Leu Ser Glu Ala Val Cys Met Lys Glu Phe
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 Asp His Pro Asn Val Met Arg Leu Ile Gly Val Cys Phe Gln Gly Ser
 595 600 605
 Glu Arg Glu Ser Phe Pro Ala Pro Val Val Ile Leu Pro Phe Met Lys
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 His Gly Asp Leu His Ser Phe Leu Leu Tyr Ser Arg Leu Gly Gly Gln
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 Ala Ser Gly Met Glu Tyr Leu Ser Thr Lys Arg Phe Ile His Arg Asp
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 Leu Ala Ala Arg Asn Cys Met Leu Asn Glu Asn Met Ser Val Cys Val
 675 680 685
 Ala Asp Phe Gly Leu Ser Lys Lys Ile Tyr Asn Gly Asp Tyr Tyr Arg
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 Gln Gly Arg Ile Ala Lys Met Pro Val Lys Trp Ile Ala Ile Glu Ser
 705 710 715 720
 Leu Ala Asp Arg Val Tyr Thr Ser Lys Ser Asp Val Trp Ser Phe Gly
 725 730 735
 Val Thr Met Trp Glu Ile Ala Thr Arg Gly Gln Thr Pro Tyr Pro Gly
 740 745 750

Val Glu Asn Ser Glu Ile Tyr Asp Tyr Leu Arg Gln Gly Asn Arg Leu
755 760 765
Lys Gln Pro Ala Asp Cys Leu Asp Gly Leu Tyr Ala Leu Met Ser Arg
770 775 780
Cys Trp Glu Leu Asn Pro Gln Asp Arg Pro Ser Phe Thr Glu Leu Arg
785 790 795 800
Glu Asp Leu Glu Asn Thr Leu Lys Ala Leu Pro Pro Ala Gln Glu Pro
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Asp Glu Ile Leu Tyr Val Asn Met Asp Glu Gly Gly Gly Tyr Pro Glu
820 825 830
Pro Pro Gly Ala Ala Gly Gly Ala Asp Pro Pro Thr Gln Pro Asp Pro
835 840 845
Lys Asp Ser Cys Ser Cys Leu Thr Ala Ala Glu Val His Pro Ala Gly
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Phe Gly Val Asn Glu Ser Thr Gly Leu Ser Leu Glu Gln Val Lys Lys
      20              25              30
ctt aag gag aga tgg ggc tcc aac gag tta ccg gct gaa gaa gga aaa  144
Leu Lys Glu Arg Trp Gly Ser Asn Glu Leu Pro Ala Glu Glu Gly Lys
      35              40              45
acc ttg ctg gaa ctt gtg att gag cag ttt gaa gac ttg cta gtt agg  192
Thr Leu Leu Glu Leu Val Ile Glu Gln Phe Glu Asp Leu Leu Val Arg
      50              55              60
att tta tta ctg gca gca tgt ata tct ttt gtt ttg gct tgg ttt gaa  240
Ile Leu Leu Leu Ala Ala Cys Ile Ser Phe Val Leu Ala Trp Phe Glu
      65              70              75
gaa ggt gaa gaa aca att aca gcc ttt gta gaa cct ttt gta att tta  288
Glu Gly Glu Glu Thr Ile Thr Ala Phe Val Glu Pro Phe Val Ile Leu
      80              85              90              95
ctc ata tta gta gcc aat gca att gtg ggt gta tgg cag gaa aga aat  336
Leu Ile Leu Val Ala Asn Ala Ile Val Gly Val Trp Gln Glu Arg Asn
      100             105             110
gct gaa aat gcc atc gaa gcc ctt aag gaa tat gag cct gaa atg ggc  384
Ala Glu Asn Ala Ile Glu Ala Leu Lys Glu Tyr Glu Pro Glu Met Gly
      115             120             125
aaa gtg tat cga cag gac aga aag agt gtg cag cgg att aaa gct aaa  432
Lys Val Tyr Arg Gln Asp Arg Lys Ser Val Gln Arg Ile Lys Ala Lys
      130             135             140

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 Pro Ala Asp Ile Arg Leu Thr Ser Ile Lys Ser Thr Thr Leu Arg Val
 160 165 170 175
 gac cag tca att ctg aca ggt gaa tct gtc tct gtc atc aag cac act 576
 Asp Gln Ser Ile Leu Thr Gly Glu Ser Val Ser Val Ile Lys His Thr
 180 185 190
 gat ccc gtc cct gac cca cga gct gtc aac caa gat aaa aag aac atg 624
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 Leu Phe Ser Gly Thr Asn Ile Ala Ala Gly Lys Ala Met Gly Val Val
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 gtg gca aca gaa cag gag aga aca ccc ctt cag caa aaa cta gat gaa 768
 Val Ala Thr Glu Gln Glu Arg Thr Pro Leu Gln Gln Lys Leu Asp Glu
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 ttt ggg gaa cag ctt tcc aaa gtc atc tcc ctt att tgc att gca gtc 816
 Phe Gly Glu Gln Leu Ser Lys Val Ile Ser Leu Ile Cys Ile Ala Val
 260 265 270
 tgg atc ata aat att ggg cac ttc aat gac ccg gtt cat gga ggg tcc 864
 Trp Ile Ile Asn Ile Gly His Phe Asn Asp Pro Val His Gly Gly Ser

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Val Ala Ala Ile Pro Glu Gly Leu Pro Ala Val Ile Thr Thr Cys Leu			
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gct ctt gga act cgc aga atg gca aag aaa aat gcc att gtt cga agc	1008		
Ala Leu Gly Thr Arg Arg Met Ala Lys Lys Asn Ala Ile Val Arg Ser			
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ctc ccg tct gtg gaa acc ctt ggt tgt act tct gtt atc tgc tca gac	1056		
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Lys Thr Gly Thr Leu Thr Thr Asn Gln Met Ser Val Cys Arg Met Phe			
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Lys Pro Val Asn Cys His Gln Tyr Asp Gly Leu Val Glu Leu Ala Thr			
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Gly Val Tyr Glu Lys Val Gly Glu Ala Thr Glu Thr Ala Leu Thr Cys			
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cta gta gag aag atg aat gta ttt gat acc gaa ttg aag ggt ctt tct			1392
Leu Val Glu Lys Met Asn Val Phe Asp Thr Glu Leu Lys Gly Leu Ser			
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465	470	475	
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Lys Lys Glu Phe Thr Leu Glu Phe Ser Arg Asp Arg Lys Ser Met Ser			
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gtt tac tgt aca cca aat aaa cca agc agg aca tca atg agc aag atg			1536
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Phe Val Lys Gly Ala Pro Glu Gly Val Ile Asp Arg Cys Thr His Ile			
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Arg Val Gly Ser Thr Lys Val Pro Met Thr Ser Gly Val Lys Gln Lys			
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Ile Met Ser Val Ile Arg Glu Trp Gly Ser Gly Ser Asp Thr Leu Arg			
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gaa cct gca ata ctg gag taaccgcttc cttaaaccatt ttgcagaaat 3024

Glu Pro Ala Ile Leu Glu

995

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<212> PRT

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Leu Leu Leu Ala Ala Cys Ile Ser Phe Val Leu Ala Trp Phe Glu Glu
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Gly Glu Glu Thr Ile Thr Ala Phe Val Glu Pro Phe Val Ile Leu Leu
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Ile Leu Val Ala Asn Ala Ile Val Gly Val Trp Gln Glu Arg Asn Ala
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Glu Asn Ala Ile Glu Ala Leu Lys Glu Tyr Glu Pro Glu Met Gly Lys
115 120 125
Val Tyr Arg Gln Asp Arg Lys Ser Val Gln Arg Ile Lys Ala Lys Asp
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Ile Val Pro Gly Asp Ile Val Glu Ile Ala Val Gly Asp Lys Val Pro
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Gln Ser Ile Leu Thr Gly Glu Ser Val Ser Val Ile Lys His Thr Asp
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Pro Val Pro Asp Pro Arg Ala Val Asn Gln Asp Lys Lys Asn Met Leu
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Phe Ser Gly Thr Asn Ile Ala Ala Gly Lys Ala Met Gly Val Val Val
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Ile Arg Gly Ala Ile Tyr Tyr Phe Lys Ile Ala Val Ala Leu Ala Val
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Pro Ser Val Glu Thr Leu Gly Cys Thr Ser Val Ile Cys Ser Asp Lys
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Thr Gly Thr Leu Thr Thr Asn Gln Met Ser Val Cys Arg Met Phe Ile
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Val Tyr Glu Lys Val Gly Glu Ala Thr Glu Thr Ala Leu Thr Cys Leu
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Val Glu Lys Met Asn Val Phe Asp Thr Glu Leu Lys Gly Leu Ser Lys
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 Lys Glu Phe Thr Leu Glu Phe Ser Arg Asp Arg Lys Ser Met Ser Val
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 Val Gly Ser Thr Lys Val Pro Met Thr Ser Gly Val Lys Gln Lys Ile
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 Met Ser Val Ile Arg Glu Trp Gly Ser Gly Ser Asp Thr Leu Arg Cys
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 580 585 590
 Val Gly Cys Val Gly Met Leu Asp Pro Pro Arg Ile Glu Val Ala Ser
 595 600 605
 Ser Val Lys Leu Cys Arg Gln Ala Gly Ile Arg Val Ile Met Ile Thr
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 Gly Asp Asn Lys Gly Thr Ala Val Ala Ile Cys Arg Arg Ile Gly Ile
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 Phe Gly Gln Asp Glu Asp Val Thr Ser Lys Ala Phe Thr Gly Arg Glu
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 660 665 670

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Arg Cys Phe Ala Arg Val Glu Pro Ser His Lys Ser Lys Ile Val Glu
 675 680 685
 Phe Leu Gln Ser Phe Asp Glu Ile Thr Ala Met Thr Gly Asp Gly Val
 690 695 700
 Asn Asp Ala Pro Ala Leu Lys Lys Ala Glu Ile Gly Ile Ala Met Gly
 705 710 715 720
 Ser Gly Thr Ala Val Ala Lys Thr Ala Ser Glu Met Val Leu Ala Asp
 725 730 735
 Asp Asn Phe Ser Thr Ile Val Ala Ala Val Glu Glu Gly Arg Ala Ile
 740 745 750
 Tyr Asn Asn Met Lys Gln Phe Ile Arg Tyr Leu Ile Ser Ser Asn Val
 755 760 765
 Gly Glu Val Val Cys Ile Phe Leu Thr Ala Ala Leu Gly Phe Pro Glu
 770 775 780
 Ala Leu Ile Pro Val Gln Leu Leu Trp Val Asn Leu Val Thr Asp Gly
 785 790 795 800
 Leu Pro Ala Thr Ala Leu Gly Phe Asn Pro Pro Asp Leu Asp Ile Met
 805 810 815
 Asn Lys Pro Pro Arg Asn Pro Lys Glu Pro Leu Ile Ser Gly Trp Leu
 820 825 830
 Phe Phe Arg Tyr Leu Ala Ile Gly Cys Tyr Val Gly Ala Ala Thr Val
 835 840 845
 Gly Ala Ala Ala Trp Trp Phe Ile Ala Ala Asp Gly Gly Pro Arg Val
 850 855 860
 Ser Phe Tyr Gln Leu Ser His Phe Leu Gln Cys Lys Glu Asp Asn Pro
 865 870 875 880
 Asp Phe Glu Gly Val Asp Cys Ala Ile Phe Glu Ser Pro Tyr Pro Met

885 890 895
Thr Met Ala Leu Ser Val Leu Val Thr Ile Glu Met Cys Asn Ala Leu
900 905 910
Asn Ser Leu Ser Glu Asn Gln Ser Leu Leu Arg Met Pro Pro Trp Glu
915 920 925
Asn Ile Trp Leu Val Gly Ser Ile Cys Leu Ser Met Ser Leu His Phe
930 935 940
Leu Ile Leu Tyr Val Glu Pro Leu Pro Leu Ile Phe Gln Ile Thr Pro
945 950 955 960
Leu Asn Val Thr Gln Trp Leu Met Val Leu Lys Ile Ser Leu Pro Val
965 970 975
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980 985 990
Pro Ala Ile Leu Glu
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<210> 29

<211> 1103

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (133).. (834)

<400> 29

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ggctcctgac ca atg ggg aag tgg cat gtg gga ggg cgc cgg ggt tcc ccc 171

Met Gly Lys Trp His Val Gly Gly Arg Arg Gly Ser Pro

1 5 10

cgc caa tgg gga gct acg gcg cgc ggc cgg gac ttg gag gcg gtg cgg 219

Arg Gln Trp Gly Ala Thr Ala Arg Gly Arg Asp Leu Glu Ala Val Arg

15 20 25

cgc ggc ggg tgc ggt tca gtc ggt cgg cgg cgg cag cgg agg agg agg 267

Arg Gly Gly Cys Gly Ser Val Gly Arg Arg Arg Gln Arg Arg Arg Arg

30 35 40 45

agg agg agg agg atg agg agg atg agg agg atg tgg gcc acg cag ggg 315

Arg Arg Arg Arg Met Arg Arg Met Arg Arg Met Trp Ala Thr Gln Gly

50 55 60

ctg gcg gtg cgc gtg gct ctg agc gtg ctg ccg ggc agc cgg gcg ctg 363

Leu Ala Val Arg Val Ala Leu Ser Val Leu Pro Gly Ser Arg Ala Leu

65 70 75

cgg ccg ggc gac tgc gaa gtt tgt att tct tat ctg gga aga ttt tac 411

Arg Pro Gly Asp Cys Glu Val Cys Ile Ser Tyr Leu Gly Arg Phe Tyr

80 85 90

cag gac ctc aaa gac aga gat gtc aca ttc tca cca gcc act att gaa 459

Gln Asp Leu Lys Asp Arg Asp Val Thr Phe Ser Pro Ala Thr Ile Glu

95 100 105

aac gaa ctt ata aag ttc tgc cgg gaa gca aga ggc aaa gag aat cgg 507

Asn Glu Leu Ile Lys Phe Cys Arg Glu Ala Arg Gly Lys Glu Asn Arg

110 115 120 125

ttg tgc tac tat atc ggg gcc aca gat gat gca gcc acc aaa atc atc 555

Leu Cys Tyr Tyr Ile Gly Ala Thr Asp Asp Ala Ala Thr Lys Ile Ile

130 135 140

aat gag gla tca aag cct ctg gcc cac cac atc cct gtg gag aag atc 603
 Asn Glu Val Ser Lys Pro Leu Ala His His Ile Pro Val Glu Lys Ile
 145 150 155
 tgt gag aag ctt aag aag aag gac agc cag ata tgt gag ctt aag tat 651
 Cys Glu Lys Leu Lys Lys Lys Asp Ser Gln Ile Cys Glu Leu Lys Tyr
 160 165 170
 gac aag cag atc gac ctg agc aca gtg gac ctg aag aag ctc cga gtt 699
 Asp Lys Gln Ile Asp Leu Ser Thr Val Asp Leu Lys Lys Leu Arg Val
 175 180 185
 aaa gag ctg aag aag att ctg gat gac tgg ggg gag aca tgc aaa ggc 747
 Lys Glu Leu Lys Lys Ile Leu Asp Asp Trp Gly Glu Thr Cys Lys Gly
 190 195 200 205
 tgt gca gaa aag tct gac tac atc cgg aag ata aat gaa ctg atg cct 795
 Cys Ala Glu Lys Ser Asp Tyr Ile Arg Lys Ile Asn Glu Leu Met Pro
 210 215 220
 aaa tat gcc ccc aag gca gcc agt gca ccg acc gat ttg tagtctgctc 844
 Lys Tyr Ala Pro Lys Ala Ala Ser Ala Pro Thr Asp Leu
 225 230
 aatctctgtt gcaccigagg gggaaaaaac agttcaactg cttaciccga aaacagcctt 904
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<211> 234

<212> PRT

<213> Homo sapiens

<400> 30

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5

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15

Gly Ala Thr Ala Arg Gly Arg Asp Leu Glu Ala Val Arg Arg Gly Gly

20

25

30

Cys Gly Ser Val Gly Arg Arg Arg Gln Arg Arg Arg Arg Arg Arg Arg

35

40

45

Arg Met Arg Arg Met Arg Arg Met Trp Ala Thr Gln Gly Leu Ala Val

50

55

60

Arg Val Ala Leu Ser Val Leu Pro Gly Ser Arg Ala Leu Arg Pro Gly

65

70

75

80

Asp Cys Glu Val Cys Ile Ser Tyr Leu Gly Arg Phe Tyr Gln Asp Leu

85

90

95

Lys Asp Arg Asp Val Thr Phe Ser Pro Ala Thr Ile Glu Asn Glu Leu

100

105

110

Ile Lys Phe Cys Arg Glu Ala Arg Gly Lys Glu Asn Arg Leu Cys Tyr

115

120

125

Tyr Ile Gly Ala Thr Asp Asp Ala Ala Thr Lys Ile Ile Asn Glu Val

130

135

140

Ser Lys Pro Leu Ala His His Ile Pro Val Glu Lys Ile Cys Glu Lys

145

150

155

160

Leu Lys Lys Lys Asp Ser Gln Ile Cys Glu Leu Lys Tyr Asp Lys Gln

165

170

175

Ile Asp Leu Ser Thr Val Asp Leu Lys Lys Leu Arg Val Lys Glu Leu

180

185

190

Lys Lys Ile Leu Asp Asp Trp Gly Glu Thr Cys Lys Gly Cys Ala Glu

195	200	205	
Lys Ser Asp Tyr Ile Arg Lys Ile Asn Glu Leu Met Pro Lys Tyr Ala			
210	215	220	
Pro Lys Ala Ala Ser Ala Pro Thr Asp Leu			
225	230		
<p><210> 31</p> <p><211> 1860</p> <p><212> DNA</p> <p><213> Homo sapiens</p> <p><220></p> <p><221> CDS</p> <p><222> (94).. (1266)</p> <p><400> 31</p>			
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tta att tat tct ggg aag ctg ttg ttg gat cac caa tgt ctc agg gac	306
Leu Ile Tyr Ser Gly Lys Leu Leu Leu Asp His Gln Cys Leu Arg Asp	
60 65 70	
ttg ctt cca aag cag gaa aaa cgg cat gtt ttg cat ctg gtg tgc aat	354
Leu Leu Pro Lys Gln Glu Lys Arg His Val Leu His Leu Val Cys Asn	
75 80 85	
gtg aag agt cct tca aaa atg cca gaa atc aac gcc aag gtg gct gaa	402
Val Lys Ser Pro Ser Lys Met Pro Glu Ile Asn Ala Lys Val Ala Glu	
90 95 100	
tcc aca gag gag cct gct ggt tct aat cgg gga cag tat cct gag gat	450
Ser Thr Glu Glu Pro Ala Gly Ser Asn Arg Gly Gln Tyr Pro Glu Asp	
105 110 115	
tcc tca agt gat ggt tta agg caa agg gaa gtt ctt cgg aac ctt tct	498
Ser Ser Ser Asp Gly Leu Arg Gln Arg Glu Val Leu Arg Asn Leu Ser	
120 125 130 135	
tcc cct gga tgg gaa aac atc tca agg cct gaa gct gcc cag cag gca	546
Ser Pro Gly Trp Glu Asn Ile Ser Arg Pro Glu Ala Ala Gln Gln Ala	
140 145 150	
ttc caa ggc ctg ggt cct ggt ttc tcc ggt tac aca ccc tat ggg tgg	594
Phe Gln Gly Leu Gly Pro Gly Phe Ser Gly Tyr Thr Pro Tyr Gly Trp	
155 160 165	
ctt cag ctt tcc tgg ttc cag cag ata tat gca cga cag tac tac atg	642
Leu Gln Leu Ser Trp Phe Gln Gln Ile Tyr Ala Arg Gln Tyr Tyr Met	
170 175 180	
caa tat tta gca gcc act gct gca tca ggg gct ttt gtt cca cca cca	690
Gln Tyr Leu Ala Ala Thr Ala Ala Ser Gly Ala Phe Val Pro Pro Pro	

185	190	195	
agl gca caa gag ata cct gtg gtc tct gca cct gct cca gcc cct att	738		
Ser Ala Gln Glu Ile Pro Val Val Ser Ala Pro Ala Pro Ala Pro Ile			
200	205	210	215
cac aac cag ttt cca gct gaa aac cag cct gcc aat cag aat gct gct	786		
His Asn Gln Phe Pro Ala Glu Asn Gln Pro Ala Asn Gln Asn Ala Ala			
220	225	230	
cct caa gtg gtt gtt aat cct gga gcc aat caa aat ttg cgg atg aat	834		
Pro Gln Val Val Val Asn Pro Gly Ala Asn Gln Asn Leu Arg Met Asn			
235	240	245	
gca caa ggt ggc cct att gtg gaa gaa gat gat gaa ata aat cga gat	882		
Ala Gln Gly Gly Pro Ile Val Glu Glu Asp Asp Glu Ile Asn Arg Asp			
250	255	260	
tgg ttg gat tgg acc tat tca gca gct aca ttt tct gtt ttt ctc agt	930		
Trp Leu Asp Trp Thr Tyr Ser Ala Ala Thr Phe Ser Val Phe Leu Ser			
265	270	275	
atc ctc tac ttc tac tcc tcc ctg agc aga ttc ctc atg gtc atg ggg	978		
Ile Leu Tyr Phe Tyr Ser Ser Leu Ser Arg Phe Leu Met Val Met Gly			
280	285	290	295
gcc acc gtt gtt atg tac ctg cat cac gtt ggg tgg ttt cca ttt aga	1026		
Ala Thr Val Val Met Tyr Leu His His Val Gly Trp Phe Pro Phe Arg			
300	305	310	
ccg agg ccg gtt cag aac ttc cca aat gat ggt cct cct cct gac gtt	1074		
Pro Arg Pro Val Gln Asn Phe Pro Asn Asp Gly Pro Pro Pro Asp Val			
315	320	325	
gta aat cag gac ccc aac aat aac tta cag gaa ggc act gat cct gaa	1122		
Val Asn Gln Asp Pro Asn Asn Asn Leu Gln Glu Gly Thr Asp Pro Glu			

330 335 340
 act gaa gac ccc aac cac ctc cct cca gac agg gat gta cta gat ggc 1170
 Thr Glu Asp Pro Asn His Leu Pro Pro Asp Arg Asp Val Leu Asp Gly
 345 350 355
 gag cag acc agc ccc tcc ttt atg agc aca gca tgg ctt gtc ttc aag 1218
 Glu Gln Thr Ser Pro Ser Phe Met Ser Thr Ala Trp Leu Val Phe Lys
 360 365 370 375
 act ttc ttt gcc tct ctt ctt cca gaa ggc ccc cca gcc atc gca aac 1266
 Thr Phe Phe Ala Ser Leu Leu Pro Glu Gly Pro Pro Ala Ile Ala Asn
 380 385 390
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<210> 32

<211> 391

<212> PRT

<213> Homo sapiens

<400> 32

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 20 25 30
 Ser Val Gly His Leu Lys Ala His Leu Ser Arg Val Tyr Pro Glu Arg
 35 40 45
 Pro Arg Pro Glu Asp Gln Arg Leu Ile Tyr Ser Gly Lys Leu Leu Leu
 50 55 60
 Asp His Gln Cys Leu Arg Asp Leu Leu Pro Lys Gln Glu Lys Arg His
 65 70 75 80
 Val Leu His Leu Val Cys Asn Val Lys Ser Pro Ser Lys Met Pro Glu
 85 90 95
 Ile Asn Ala Lys Val Ala Glu Ser Thr Glu Glu Pro Ala Gly Ser Asn
 100 105 110
 Arg Gly Gln Tyr Pro Glu Asp Ser Ser Ser Asp Gly Leu Arg Gln Arg
 115 120 125
 Glu Val Leu Arg Asn Leu Ser Ser Pro Gly Trp Glu Asn Ile Ser Arg
 130 135 140
 Pro Glu Ala Ala Gln Gln Ala Phe Gln Gly Leu Gly Pro Gly Phe Ser
 145 150 155 160
 Gly Tyr Thr Pro Tyr Gly Trp Leu Gln Leu Ser Trp Phe Gln Gln Ile
 165 170 175
 Tyr Ala Arg Gln Tyr Tyr Met Gln Tyr Leu Ala Ala Thr Ala Ala Ser
 180 185 190
 Gly Ala Phe Val Pro Pro Pro Ser Ala Gln Glu Ile Pro Val Val Ser
 195 200 205
 Ala Pro Ala Pro Ala Pro Ile His Asn Gln Phe Pro Ala Glu Asn Gln

210 215 220
Pro Ala Asn Gln Asn Ala Ala Pro Gln Val Val Val Asn Pro Gly Ala
225 230 235 240
Asn Gln Asn Leu Arg Met Asn Ala Gln Gly Gly Pro Ile Val Glu Glu
245 250 255
Asp Asp Glu Ile Asn Arg Asp Trp Leu Asp Trp Thr Tyr Ser Ala Ala
260 265 270
Thr Phe Ser Val Phe Leu Ser Ile Leu Tyr Phe Tyr Ser Ser Leu Ser
275 280 285
Arg Phe Leu Met Val Met Gly Ala Thr Val Val Met Tyr Leu His His
290 295 300
Val Gly Trp Phe Pro Phe Arg Pro Arg Pro Val Gln Asn Phe Pro Asn
305 310 315 320
Asp Gly Pro Pro Pro Asp Val Val Asn Gln Asp Pro Asn Asn Asn Leu
325 330 335
Gln Glu Gly Thr Asp Pro Glu Thr Glu Asp Pro Asn His Leu Pro Pro
340 345 350
Asp Arg Asp Val Leu Asp Gly Glu Gln Thr Ser Pro Ser Phe Met Ser
355 360 365
Thr Ala Trp Leu Val Phe Lys Thr Phe Phe Ala Ser Leu Leu Pro Glu
370 375 380
Gly Pro Pro Ala Ile Ala Asn
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<210> 33

<211> 4067

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (812).. (1138)

<400> 33

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 cgccacccta ggaggcgcg tgcacccac tactctgtcc tctgctgtg ctccgtgccc 180
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 cctatcacct catctccga aaggctcagg gcagctccgg ggcggctcag gcgaagcggc 780
 tgcagcggcg gtagcggcg cgggaggcag g atg agc gca cgc ggt gag ggc 832

Met Ser Ala Arg Gly Glu Gly

1

5

gcg ggg cag ccg tcc act tca gcc cag gga caa cct gcc gcc cca gcg 880

Ala Gly Gln Pro Ser Thr Ser Ala Gln Gly Gln Pro Ala Ala Pro Ala

10

15

20

cct cag aag aga gga cgc ggc cgc ccc agg aag cag cag caa gaa cca 928

Pro Gln Lys Arg Gly Arg Gly Arg Pro Arg Lys Gln Gln Gln Glu Pro

25

30

35

acc ggt gag ccc tct cct aag aga ccc agg gga aga ccc aaa ggc agc 976
 Thr Gly Glu Pro Ser Pro Lys Arg Pro Arg Gly Arg Pro Lys Gly Ser
 40 45 50 55
 aaa aac aag agt ccc tct aaa gca gct caa aag aaa gca gaa gcc act 1024
 Lys Asn Lys Ser Pro Ser Lys Ala Ala Gln Lys Lys Ala Glu Ala Thr
 60 65 70
 gga gaa aaa cgg cca aga ggc aga cct agg aaa tgg cca caa caa gtt 1072
 Gly Glu Lys Arg Pro Arg Gly Arg Pro Arg Lys Trp Pro Gln Gln Val
 75 80 85
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 Val Gln Lys Lys Pro Ala Gln Glu Glu Thr Glu Glu Thr Ser Ser Gln
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 gag tct gcc gaa gag gac tagggggcgc aacgttcgat ttctacctca 1168
 Glu Ser Ala Glu Glu Asp
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 taacagcctc tgtgatccc 4067

<210> 34

<211> 109

<212> PRT

<213> Homo sapiens

<400> 34

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Gly Gln Pro Ala Ala Pro Ala Pro Gln Lys Arg Gly Arg Gly Arg Pro

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Arg Lys Gln Gln Gln Glu Pro Thr Gly Glu Pro Ser Pro Lys Arg Pro

35 40 45

Arg Gly Arg Pro Lys Gly Ser Lys Asn Lys Ser Pro Ser Lys Ala Ala

50 55 60

Gln Lys Lys Ala Glu Ala Thr Gly Glu Lys Arg Pro Arg Gly Arg Pro

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Thr Glu Glu Thr Ser Ser Gln Glu Ser Ala Glu Glu Asp

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105

<210> 35

<211> 4228

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (148).. (1032)

<400> 35

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cccagctgcc caggaagagc cccagcc atg gaa cac cag ctc ctg tgc tgc gaa 174

Met Glu His Gln Leu Leu Cys Cys Glu

1

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Val Glu Thr Ile Arg Arg Ala Tyr Pro Asp Ala Asn Leu Leu Asn Asp

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cgg gtg ctg cgg gcc atg ctg aag gcg gag gag acc tgc gcg ccc tcg 270

Arg Val Leu Arg Ala Met Leu Lys Ala Glu Glu Thr Cys Ala Pro Ser

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Val Ser Tyr Phe Lys Cys Val Gln Lys Glu Val Leu Pro Ser Met Arg

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Lys Ile Val Ala Thr Trp Met Leu Glu Val Cys Glu Glu Gln Lys Cys
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Val Ala Leu Cys Ala Thr Asp Val Lys Phe Ile Ser Asn Pro Pro Ser

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Met Val Ala Ala Gly Ser Val Val Ala Ala Val Gln Gly Leu Asn Leu			
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agg agc ccc aac aac ttc ctg tcc tac tac cgc ctc aca cgc ttc ctc			846
Arg Ser Pro Asn Asn Phe Leu Ser Tyr Tyr Arg Leu Thr Arg Phe Leu			
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Gln Ile Glu Ala Leu Leu Glu Ser Ser Leu Arg Gln Ala Gln Gln Asn			
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Lys Ala Glu Glu Thr Cys Ala Pro Ser Val Ser Tyr Phe Lys Cys Val			
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Gln Lys Glu Val Leu Pro Ser Met Arg Lys Ile Val Ala Thr Trp Met			
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Leu Glu Val Cys Glu Glu Gln Lys Cys Glu Glu Glu Val Phe Pro Leu			
65	70	75	80
Ala Met Asn Tyr Leu Asp Arg Phe Leu Ser Leu Glu Pro Val Lys Lys			
85	90	95	
Ser Arg Leu Gln Leu Leu Gly Ala Thr Cys Met Phe Val Ala Ser Lys			
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Met Lys Glu Thr Ile Pro Leu Thr Ala Glu Lys Leu Cys Ile Tyr Thr			
115	120	125	
Asp Asn Ser Ile Arg Pro Glu Glu Leu Leu Gln Met Glu Leu Leu Leu			
130	135	140	
Val Asn Lys Leu Lys Trp Asn Leu Ala Ala Met Thr Pro His Asp Phe			
145	150	155	160
Ile Glu His Phe Leu Ser Lys Met Pro Glu Ala Glu Glu Asn Lys Gln			
165	170	175	
Ile Ile Arg Lys His Ala Gln Thr Phe Val Ala Leu Cys Ala Thr Asp			
180	185	190	
Val Lys Phe Ile Ser Asn Pro Pro Ser Met Val Ala Ala Gly Ser Val			
195	200	205	
Val Ala Ala Val Gln Gly Leu Asn Leu Arg Ser Pro Asn Asn Phe Leu			
210	215	220	

Ser Tyr Tyr Arg Leu Thr Arg Phe Leu Ser Arg Val Ile Lys Cys Asp
 225 230 235 240
 Pro Asp Cys Leu Arg Ala Cys Gln Glu Gln Ile Glu Ala Leu Leu Glu
 245 250 255
 Ser Ser Leu Arg Gln Ala Gln Gln Asn Met Asp Pro Lys Ala Ala Glu
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Met Lys Gly Leu Gly Asp Ser Arg Pro Arg His Leu

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Ser Asp Ser Leu Asp Pro Pro His Glu Pro Leu Phe Ala Gly Thr Asp

15 20 25

cgc aac ccc tac ctg ctg tgc ccc acg gag gcc ttc gcc cgc gag gcc 567

Arg Asn Pro Tyr Leu Leu Ser Pro Thr Glu Ala Phe Ala Arg Glu Ala

30 35 40

cgc ttc ccc ggg cag aac acc ctg cca gga gat ggc ctc ttt ccc ctc 615

Arg Phe Pro Gly Gln Asn Thr Leu Pro Gly Asp Gly Leu Phe Pro Leu

45 50 55 60

aac aac cag ctg ccc ccg ccc agc agc acc ttt ccc cgc atc cac tac 663

Asn Asn Gln Leu Pro Pro Pro Ser Ser Thr Phe Pro Arg Ile His Tyr

65 70 75

aac tcc cac ttc gag gtg cca gag gag agc ccc ttc ccc agc cat gcc 711

Asn Ser His Phe Glu Val Pro Glu Glu Ser Pro Phe Pro Ser His Ala

80 85 90

caa gcc acc aag atc aac cgg ctg ccc gcc aac ctc ctg gac cag ttt 759

Gln Ala Thr Lys Ile Asn Arg Leu Pro Ala Asn Leu Leu Asp Gln Phe

95 100 105

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Glu Lys Gln Leu Pro Ile His Arg Asp Gly Phe Ser Thr Leu Gln Phe

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ccc cgt ggc gag gcc aag gcc cgt ggt gag agc cct ggc cgc atc cgc 855

Pro Arg Gly Glu Ala Lys Ala Arg Gly Glu Ser Pro Gly Arg Ile Arg

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 His Leu Val His Ser Val Gln Arg Leu Phe Phe Thr Lys Ala Pro Ser
 145 150 155
 ctg gag ggc aca gcg ggc aag gtc ggt ggc aat ggc agc aag aag ggt 951
 Leu Glu Gly Thr Ala Gly Lys Val Gly Gly Asn Gly Ser Lys Lys Gly
 160 165 170
 ggc atg gag gac ggc aag ggc cgg agg gcc aaa agc aag gag cgg gcc 999
 Gly Met Glu Asp Gly Lys Gly Arg Arg Ala Lys Ser Lys Glu Arg Ala
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 Lys Ala Gly Glu Pro Lys Arg Arg Ser Arg Ser Asn Ile Ser Gly Trp
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 Trp Ser Ser Asp Asp Asn Leu Asp Gly Glu Ala Gly Ala Phe Arg Ser
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 Ser Gln Pro Arg Tyr Phe Met His Ala Tyr Asn Thr Ile Ser Gly His
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 Met Leu Lys Thr Thr Lys Asn Asn Thr Thr Glu Leu Thr Ala Pro Pro
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 ccc ccg ccc gca ccc cca gcc acc tgc ccc agc ctt ggg gtg ggc act 1287
 Pro Pro Pro Ala Pro Pro Ala Thr Cys Pro Ser Leu Gly Val Gly Thr
 270 275 280

gac acc aac tac gtc aaa cgg ggc tcc tgg tcc act ctg acc ctc agc 1335
 Asp Thr Asn Tyr Val Lys Arg Gly Ser Trp Ser Thr Leu Thr Leu Ser
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Lys Cys Pro Ser Trp Glu Glu Asp Tyr Thr Pro Val Ser Asp Ser Leu			
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Asn Asp Ser Ser Cys Ile Ser Gln Ile Phe Gly Gln Ala Ser Leu Ile			
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ccc cag ttg ttt ggc cat gag cag cag gta cgg gag gca gag ctg agt			1863
Pro Gln Leu Phe Gly His Glu Gln Gln Val Arg Glu Ala Glu Leu Ser			
	465	470	475
gac cag tat gag gcg gcc tgc gag tca gcc tgc agt gaa gcg gag tcc			1911
Asp Gln Tyr Glu Ala Ala Cys Glu Ser Ala Cys Ser Glu Ala Glu Ser			
480	485	490	
aca gcg gca gag acg ctt gac ttg cca ctg ccc agc tac ttc cgc tcc			1959
Thr Ala Ala Glu Thr Leu Asp Leu Pro Leu Pro Ser Tyr Phe Arg Ser			
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Glu Asp Ser Val Ser Leu Gln Ser Leu Ser Pro Pro Pro Ser Thr Gly			
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Tyr Lys Lys Thr Pro Pro Pro Val Pro Pro Arg Thr Thr Ser Lys Pro			

560	565	570	
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Ile Gln Glu Arg Thr Arg Arg Asn Gly Ser His Leu Ser Glu Asp Asn			
670	675	680	
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 765 770 775 780
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 Leu Glu Thr Ser Ser Ser Ser Pro Ala Glu Pro Ala Gln Pro Gly Ala
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 Glu Arg Leu Glu Gly Trp Cys Cys Gln Met Asp Lys Glu Thr Lys Glu
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 830 835 840
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Ser Ala Gln Leu Leu Met Ser Gln Lys Phe Gln Gln Phe Arg Gly Leu
 845 850 855 860
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 Cys Glu Gln Asn Leu Asn Pro Asp Ala Asn Pro Arg Pro Thr Ala Gln
 865 870 875
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cctgcccttt tattttctcc agccccctct tcttcagca aaatctagga ctcccagatg 4232

gcttccaggg ggccgtcagt cctcagccgc gccgtgttcc ggtgcccag gggcggggcg 4292

cggtgtctgt atgtatgtgt acatatgcac atagacctta gattgtatag ttaacaaacg 4352

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ggaggcgggt gtgtgaatag catatatatt tacatgtact atatctaggt gtgtgtacaa 4472

gtgtgtgtaa aaatatatac ctgtgtgtga agcagccctt ttttttttg gtctccacc 4532

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<210> 38

<211> 989

<212> PRT

<213> Homo sapiens

<400> 38

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Asp Pro Pro His Glu Pro Leu Phe Ala Gly Thr Asp Arg Asn Pro Tyr

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Leu Leu Ser Pro Thr Glu Ala Phe Ala Arg Glu Ala Arg Phe Pro Gly

35 40 45

Gln Asn Thr Leu Pro Gly Asp Gly Leu Phe Pro Leu Asn Asn Gln Leu

50 55 60

Pro Pro Pro Ser Ser Thr Phe Pro Arg Ile His Tyr Asn Ser His Phe

65 70 75 80

Glu Val Pro Glu Glu Ser Pro Phe Pro Ser His Ala Gln Ala Thr Lys

85 90 95

Ile Asn Arg Leu Pro Ala Asn Leu Leu Asp Gln Phe Glu Lys Gln Leu

100 105 110

Pro Ile His Arg Asp Gly Phe Ser Thr Leu Gln Phe Pro Arg Gly Glu

115 120 125

Ala Lys Ala Arg Gly Glu Ser Pro Gly Arg Ile Arg His Leu Val His

130 135 140

Ser Val Gln Arg Leu Phe Phe Thr Lys Ala Pro Ser Leu Glu Gly Thr

145 150 155 160

Ala Gly Lys Val Gly Gly Asn Gly Ser Lys Lys Gly Gly Met Glu Asp
 165 170 175
 Gly Lys Gly Arg Arg Ala Lys Ser Lys Glu Arg Ala Lys Ala Gly Glu
 180 185 190
 Pro Lys Arg Arg Ser Arg Ser Asn Ile Ser Gly Trp Trp Ser Ser Asp
 195 200 205
 Asp Asn Leu Asp Gly Glu Ala Gly Ala Phe Arg Ser Ser Gly Pro Ala
 210 215 220
 Ser Gly Leu Met Ile Leu Gly Arg Gln Ala Glu Arg Ser Gln Pro Arg
 225 230 235 240
 Tyr Phe Met His Ala Tyr Asn Thr Ile Ser Gly His Met Leu Lys Thr
 245 250 255
 Thr Lys Asn Asn Thr Thr Glu Leu Thr Ala Pro Pro Pro Pro Pro Ala
 260 265 270
 Pro Pro Ala Thr Cys Pro Ser Leu Gly Val Gly Thr Asp Thr Asn Tyr
 275 280 285
 Val Lys Arg Gly Ser Trp Ser Thr Leu Thr Leu Ser His Ala His Glu
 290 295 300
 Val Cys Gln Lys Thr Ser Ala Thr Leu Asp Lys Ser Leu Leu Lys Ser
 305 310 315 320
 Lys Ser Cys His Gln Gly Leu Ala Tyr His Tyr Leu Gln Val Pro Gly
 325 330 335
 Gly Gly Gly Glu Trp Ser Thr Thr Leu Leu Ser Pro Arg Glu Thr Asp
 340 345 350
 Ala Ala Ala Glu Gly Pro Ile Pro Cys Arg Arg Met Arg Ser Gly Ser
 355 360 365

Tyr Ile Lys Ala Met Gly Asp Glu Asp Ser Asp Glu Ser Gly Gly Ser
 370 375 380
 Pro Lys Pro Ser Pro Lys Thr Ala Ala Arg Arg Gln Ser Tyr Leu Arg
 385 390 395 400
 Ala Thr Gln Gln Ser Leu Gly Glu Gln Ser Asn Pro Arg Arg Ser Leu
 405 410 415
 Asp Arg Leu Asp Ser Val Asp Met Leu Leu Pro Ser Lys Cys Pro Ser
 420 425 430
 Trp Glu Glu Asp Tyr Thr Pro Val Ser Asp Ser Leu Asn Asp Ser Ser
 435 440 445
 Cys Ile Ser Gln Ile Phe Gly Gln Ala Ser Leu Ile Pro Gln Leu Phe
 450 455 460
 Gly His Glu Gln Gln Val Arg Glu Ala Glu Leu Ser Asp Gln Tyr Glu
 465 470 475 480
 Ala Ala Cys Glu Ser Ala Cys Ser Glu Ala Glu Ser Thr Ala Ala Glu
 485 490 495
 Thr Leu Asp Leu Pro Leu Pro Ser Tyr Phe Arg Ser Arg Ser His Ser
 500 505 510
 Tyr Leu Arg Ala Ile Gln Ala Gly Cys Ser Gln Glu Glu Asp Ser Val
 515 520 525
 Ser Leu Gln Ser Leu Ser Pro Pro Pro Ser Thr Gly Ser Leu Ser Asn
 530 535 540
 Ser Arg Thr Leu Pro Ser Ser Ser Cys Leu Val Ala Tyr Lys Lys Thr
 545 550 555 560
 Pro Pro Pro Val Pro Pro Arg Thr Thr Ser Lys Pro Phe Ile Ser Val
 565 570 575
 Thr Val Gln Ser Ser Thr Glu Ser Ala Gln Asp Thr Tyr Leu Asp Ser

580 585 590
Gln Asp His Lys Ser Glu Val Thr Ser Gln Ser Gly Leu Ser Asn Ser
595 600 605
Ser Asp Ser Leu Asp Ser Ser Thr Arg Pro Pro Ser Val Thr Arg Gly
610 615 620
Gly Val Ala Pro Ala Pro Glu Ala Pro Glu Pro Pro Pro Lys His Ala
625 630 635 640
Ala Leu Lys Ser Glu Gln Gly Thr Leu Thr Ser Ser Glu Ser His Pro
645 650 655
Glu Ala Ala Pro Lys Arg Lys Leu Ser Ser Ile Gly Ile Gln Glu Arg
660 665 670
Thr Arg Arg Asn Gly Ser His Leu Ser Glu Asp Asn Gly Pro Lys Ala
675 680 685
Ile Asp Val Met Ala Pro Ser Ser Glu Ser Ser Val Pro Ser His Ser
690 695 700
Met Ser Ser Arg Arg Asp Thr Asp Ser Asp Thr Gln Asp Ala Asn Asp
705 710 715 720
Ser Ser Cys Lys Ser Ser Glu Arg Ser Leu Pro Asp Cys Thr Pro His
725 730 735
Pro Asn Ser Ile Ser Ile Asp Ala Gly Pro Arg Gln Ala Pro Lys Ile
740 745 750
Ala Gln Ile Lys Arg Asn Leu Ser Tyr Gly Asp Asn Ser Asp Pro Ala
755 760 765
Leu Glu Ala Ser Ser Leu Pro Pro Pro Asp Pro Trp Leu Glu Thr Ser
770 775 780
Ser Ser Ser Pro Ala Glu Pro Ala Gln Pro Gly Ala Cys Arg Arg Asp

785 790 795 800
Gly Tyr Trp Phe Leu Lys Leu Leu Gln Ala Glu Thr Glu Arg Leu Glu
 805 810 815
Gly Trp Cys Cys Gln Met Asp Lys Glu Thr Lys Glu Asn Asn Leu Ser
 820 825 830
Glu Glu Val Leu Gly Lys Val Leu Ser Ala Val Gly Ser Ala Gln Leu
 835 840 845
Leu Met Ser Gln Lys Phe Gln Gln Phe Arg Gly Leu Cys Glu Gln Asn
 850 855 860
Leu Asn Pro Asp Ala Asn Pro Arg Pro Thr Ala Gln Asp Leu Ala Gly
865 870 875 880
Phe Trp Asp Leu Leu Gln Leu Ser Ile Glu Asp Ile Ser Met Lys Phe
 885 890 895
Asp Glu Leu Tyr His Leu Lys Ala Asn Ser Trp Gln Leu Val Glu Thr
 900 905 910
Pro Glu Lys Arg Lys Glu Glu Lys Lys Pro Pro Pro Pro Val Pro Lys
 915 920 925
Lys Pro Ala Lys Ser Lys Pro Ala Val Ser Arg Asp Lys Ala Ser Asp
 930 935 940
Ala Ser Asp Lys Gln Arg Gln Glu Ala Arg Lys Arg Leu Leu Ala Ala
945 950 955 960
Lys Arg Ala Ala Ser Val Arg Gln Asn Ser Ala Thr Glu Ser Ala Asp
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Ser Ile Glu Ile Tyr Val Pro Glu Ala Gln Thr Arg Leu
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<210> 39

<211> 2522

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1).. (1545)

<400> 39

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1

5

10

15

cgg ggc cag gtg gcc aag ctt gag gca gcc cta ggt gag gcc aag aag 96

Arg Gly Gln Val Ala Lys Leu Glu Ala Ala Leu Gly Glu Ala Lys Lys

20

25

30

caa ctt cag gat gag atg ctg cgg cgg gtg gat gct gag aac agg ctg 144

Gln Leu Gln Asp Glu Met Leu Arg Arg Val Asp Ala Glu Asn Arg Leu

35

40

45

cag acc atg aag gag gaa ctg gac ttc cag aag aac atc tac agt gag 192

Gln Thr Met Lys Glu Glu Leu Asp Phe Gln Lys Asn Ile Tyr Ser Glu

50

55

60

gag ctg cgt gag acc aag cgc cgt cat gag acc cga ctg gtg gag att 240

Glu Leu Arg Glu Thr Lys Arg Arg His Glu Thr Arg Leu Val Glu Ile

65

70

75

80

gac aat ggg aag cag cgt gag ttt gag agc cgg ctg gcg gat gcg ctg 288

Asp Asn Gly Lys Gln Arg Glu Phe Glu Ser Arg Leu Ala Asp Ala Leu

85

90

95

cag gaa ctg cgg gcc cag cat gag gac cag gtg gag cag tat aag aag 336

Gln Glu Leu Arg Ala Gln His Glu Asp Gln Val Glu Gln Tyr Lys Lys

100	105	110	
gag ctg gag aag act tat tct gcc aag ctg gac aat gcc agg cag tct			384
Glu Leu Glu Lys Thr Tyr Ser Ala Lys Leu Asp Asn Ala Arg Gln Ser			
115	120	125	
gct gag agg aac agc aac ctg gtg ggg gct gcc cac gag gag ctg cag			432
Ala Glu Arg Asn Ser Asn Leu Val Gly Ala Ala His Glu Glu Leu Gln			
130	135	140	
cag tgc cgc atc cgc atc gac agc ctc tct gcc cag ctc agc cag ctc			480
Gln Ser Arg Ile Arg Ile Asp Ser Leu Ser Ala Gln Leu Ser Gln Leu			
145	150	155	160
cag aag cag ctg gca gcc aag gag gcg aag ctt cga gac ctg gag gac			528
Gln Lys Gln Leu Ala Ala Lys Glu Ala Lys Leu Arg Asp Leu Glu Asp			
165	170	175	
tca ctg gcc cgt gag cgg gac acc agc cgg cgg ctg ctg gcg gaa aag			576
Ser Leu Ala Arg Glu Arg Asp Thr Ser Arg Arg Leu Leu Ala Glu Lys			
180	185	190	
gag cgg gag atg gcc gag atg cgg gca agg atg cag cag cag ctg gac			624
Glu Arg Glu Met Ala Glu Met Arg Ala Arg Met Gln Gln Gln Leu Asp			
195	200	205	
gag tac cag gag ctt ctg gac atc aag ctg gcc ctg gac atg gag atc			672
Glu Tyr Gln Glu Leu Leu Asp Ile Lys Leu Ala Leu Asp Met Glu Ile			
210	215	220	
cac gcc tac cgc aag ctc ttg gag ggc gag gag gag agg cta cgc ctg			720
His Ala Tyr Arg Lys Leu Leu Glu Gly Glu Glu Glu Arg Leu Arg Leu			
225	230	235	240
tcc ccc agc cct acc tcg cag cgc agc cgt ggc cgt gct tcc tct cac			768

Ser Pro Ser Pro Thr Ser Gln Arg Ser Arg Gly Arg Ala Ser Ser His
 245 250 255
 tca tcc cag aca cag ggt ggg ggc agc gtc acc aaa aag cgc aaa ctg 816
 Ser Ser Gln Thr Gln Gly Gly Gly Ser Val Thr Lys Lys Arg Lys Leu
 260 265 270
 gag tcc act gag agc cgc agc agc ttc tca cag cac gca cgc act agc 864
 Glu Ser Thr Glu Ser Arg Ser Ser Phe Ser Gln His Ala Arg Thr Ser
 275 280 285
 ggg cgc gtg gcc gtg gag gag gtg gat gag gag ggc aag ttt gtc cgg 912
 Gly Arg Val Ala Val Glu Glu Val Asp Glu Glu Gly Lys Phe Val Arg
 290 295 300
 ctg cgc aac aag tcc aat gag gac cag tcc atg ggc aat tgg cag atc 960
 Leu Arg Asn Lys Ser Asn Glu Asp Gln Ser Met Gly Asn Trp Gln Ile
 305 310 315 320
 aag cgc cag aat gga gat gat ccc ttg ctg act tac cgg ttc cca cca 1008
 Lys Arg Gln Asn Gly Asp Asp Pro Leu Leu Thr Tyr Arg Phe Pro Pro
 325 330 335
 aag ttc acc ctg aag gct ggg cag gtg gtg acg atc tgg gct gca gga 1056
 Lys Phe Thr Leu Lys Ala Gly Gln Val Val Thr Ile Trp Ala Ala Gly
 340 345 350
 gct ggg gcc acc cac agc ccc cct acc gac ctg gtg tgg aag gca cag 1104
 Ala Gly Ala Thr His Ser Pro Pro Thr Asp Leu Val Trp Lys Ala Gln
 355 360 365
 aac acc tgg ggc tgc ggg aac agc ctg cgt acg gct ctc atc aac tcc 1152
 Asn Thr Trp Gly Cys Gly Asn Ser Leu Arg Thr Ala Leu Ile Asn Ser
 370 375 380
 act ggg gaa gaa gtg gcc atg cgc aag ctg gtg cgc tca gtg act gtg 1200

Thr Gly Glu Glu Val Ala Met Arg Lys Leu Val Arg Ser Val Thr Val
 385 390 395 400
 gtt gag gac gac gag gat gag gat gga gat gac ctg ctc cat cac cac 1248
 Val Glu Asp Asp Glu Asp Glu Asp Gly Asp Asp Leu Leu His His His
 405 410 415
 cac ggc tcc cac tgc agc agc tcg ggg gac ccc gct gag tac aac ctg 1296
 His Gly Ser His Cys Ser Ser Ser Gly Asp Pro Ala Glu Tyr Asn Leu
 420 425 430
 cgc tcg cgc acc gtg ctg tgc ggg acc tgc ggg cag cct gcc gac aag 1344
 Arg Ser Arg Thr Val Leu Cys Gly Thr Cys Gly Gln Pro Ala Asp Lys
 435 440 445
 gca tct gcc agc ggc tca gga gcc cag gtg ggc gga ccc atc tcc tct 1392
 Ala Ser Ala Ser Gly Ser Gly Ala Gln Val Gly Gly Pro Ile Ser Ser
 450 455 460
 ggc tct tct gcc tcc agt gtc acg gtc act cgc agc tac cgc agt gtg 1440
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 465 470 475 480
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 Gly Gly Ser Gly Gly Gly Ser Phe Gly Asp Asn Leu Val Thr Arg Ser
 485 490 495
 tac ctc ctg ggc aac tcc agc ccc cga acc cag agc ccc cag aac tgc 1536
 Tyr Leu Leu Gly Asn Ser Ser Pro Arg Thr Gln Ser Pro Gln Asn Cys
 500 505 510
 agc atc atg taatctggga cctgccaggc aggggtgggg gtggaggctt 1585
 Ser Ile Met
 515

cctgcgacct cctcaccica tgcccacccc ctgccctgca cgtcatggga gggggcliga 1645
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<211> 515

<212> PRT

<213> Homo sapiens

<400> 40

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Arg Gly Gln Val Ala Lys Leu Glu Ala Ala Leu Gly Glu Ala Lys Lys

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30

Gln Leu Gln Asp Glu Met Leu Arg Arg Val Asp Ala Glu Asn Arg Leu

35 40 45
 Gln Thr Met Lys Glu Glu Leu Asp Phe Gln Lys Asn Ile Tyr Ser Glu
 50 55 60
 Glu Leu Arg Glu Thr Lys Arg Arg His Glu Thr Arg Leu Val Glu Ile
 65 70 75 80
 Asp Asn Gly Lys Gln Arg Glu Phe Glu Ser Arg Leu Ala Asp Ala Leu
 85 90 95
 Gln Glu Leu Arg Ala Gln His Glu Asp Gln Val Glu Gln Tyr Lys Lys
 100 105 110
 Glu Leu Glu Lys Thr Tyr Ser Ala Lys Leu Asp Asn Ala Arg Gln Ser
 115 120 125
 Ala Glu Arg Asn Ser Asn Leu Val Gly Ala Ala His Glu Glu Leu Gln
 130 135 140
 Gln Ser Arg Ile Arg Ile Asp Ser Leu Ser Ala Gln Leu Ser Gln Leu
 145 150 155 160
 Gln Lys Gln Leu Ala Ala Lys Glu Ala Lys Leu Arg Asp Leu Glu Asp
 165 170 175
 Ser Leu Ala Arg Glu Arg Asp Thr Ser Arg Arg Leu Leu Ala Glu Lys
 180 185 190
 Glu Arg Glu Met Ala Glu Met Arg Ala Arg Met Gln Gln Gln Leu Asp
 195 200 205
 Glu Tyr Gln Glu Leu Leu Asp Ile Lys Leu Ala Leu Asp Met Glu Ile
 210 215 220
 His Ala Tyr Arg Lys Leu Leu Glu Gly Glu Glu Glu Arg Leu Arg Leu
 225 230 235 240
 Ser Pro Ser Pro Thr Ser Gln Arg Ser Arg Gly Arg Ala Ser Ser His
 245 250 255

Ser Ser Gln Thr Gln Gly Gly Gly Ser Val Thr Lys Lys Arg Lys Leu
 260 265 270
 Glu Ser Thr Glu Ser Arg Ser Ser Phe Ser Gln His Ala Arg Thr Ser
 275 280 285
 Gly Arg Val Ala Val Glu Glu Val Asp Glu Glu Gly Lys Phe Val Arg
 290 295 300
 Leu Arg Asn Lys Ser Asn Glu Asp Gln Ser Met Gly Asn Trp Gln Ile
 305 310 315 320
 Lys Arg Gln Asn Gly Asp Asp Pro Leu Leu Thr Tyr Arg Phe Pro Pro
 325 330 335
 Lys Phe Thr Leu Lys Ala Gly Gln Val Val Thr Ile Trp Ala Ala Gly
 340 345 350
 Ala Gly Ala Thr His Ser Pro Pro Thr Asp Leu Val Trp Lys Ala Gln
 355 360 365
 Asn Thr Trp Gly Cys Gly Asn Ser Leu Arg Thr Ala Leu Ile Asn Ser
 370 375 380
 Thr Gly Glu Glu Val Ala Met Arg Lys Leu Val Arg Ser Val Thr Val
 385 390 395 400
 Val Glu Asp Asp Glu Asp Glu Asp Gly Asp Asp Leu Leu His His His
 405 410 415
 His Gly Ser His Cys Ser Ser Ser Gly Asp Pro Ala Glu Tyr Asn Leu
 420 425 430
 Arg Ser Arg Thr Val Leu Cys Gly Thr Cys Gly Gln Pro Ala Asp Lys
 435 440 445
 Ala Ser Ala Ser Gly Ser Gly Ala Gln Val Gly Gly Pro Ile Ser Ser
 450 455 460

Gly Ser Ser Ala Ser Ser Val Thr Val Thr Arg Ser Tyr Arg Ser Val

465 470 475 480

Gly Gly Ser Gly Gly Gly Ser Phe Gly Asp Asn Leu Val Thr Arg Ser

485 490 495

Tyr Leu Leu Gly Asn Ser Ser Pro Arg Thr Gln Ser Pro Gln Asn Cys

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Ser Ile Met

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<210> 41

<211> 3474

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (78).. (2813)

<400> 41

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Met Val Asp Tyr His Ala Ala Asn Gln Ser Tyr

1 5 10

cag tac ggc ccc agc agc gcg gca atg gct tgg cgg cgg ggg agc atg 158

Gln Tyr Gly Pro Ser Ser Ala Ala Met Ala Trp Arg Arg Gly Ser Met

15 20 25

ggc gac tac atg gcc cag gag gac gac tgg gac cgg gac ctg ctg ctg 206

Gly Asp Tyr Met Ala Gln Glu Asp Asp Trp Asp Arg Asp Leu Leu Leu

30 35 40

gac ccg gcc tgg gag aag cag cag cgc aag acc ttc acg gca tgg agc 254
 Asp Pro Ala Trp Glu Lys Gln Gln Arg Lys Thr Phe Thr Ala Trp Ser
 45 50 55
 aac tcc cac ctg cgg aag gca ggc aca cag atc gag aac att gat gag 302
 Asn Ser His Leu Arg Lys Ala Gly Thr Gln Ile Glu Asn Ile Asp Glu
 60 65 70 75
 gac ttc cga gac ggg ctc aag ctc atg ctg ctc ctg gag gtc ata tca 350
 Asp Phe Arg Asp Gly Leu Lys Leu Met Leu Leu Leu Glu Val Ile Ser
 80 85 90
 ggg gag cgg tta cct aag ccg gag cgg ggg aag atg aga gtg cac aaa 398
 Gly Glu Arg Leu Pro Lys Pro Glu Arg Gly Lys Met Arg Val His Lys
 95 100 105
 atc aac aat gtg aac aaa gcg ctg gac ttt att gcc agc aaa ggg atc 446
 Ile Asn Asn Val Asn Lys Ala Leu Asp Phe Ile Ala Ser Lys Gly Ile
 110 115 120
 aag ctg gac ttc cat cgg gca gaa gag att gtg gac ggc aac gca aag 494
 Lys Leu Asp Phe His Arg Ala Glu Glu Ile Val Asp Gly Asn Ala Lys
 125 130 135
 atg acc ctg gga atg atc tgg acc atc atc ctt agg ttc gcc atc cag 542
 Met Thr Leu Gly Met Ile Trp Thr Ile Ile Leu Arg Phe Ala Ile Gln
 140 145 150 155
 gac atc tcc gtg gaa gag acc tcg gcc aag gaa ggg ctc ctt ctc tgg 590
 Asp Ile Ser Val Glu Glu Thr Ser Ala Lys Glu Gly Leu Leu Leu Trp
 160 165 170
 tgc cag aga aag aca gcc cca tat aag aac gtc aat gtg cag aac ttc 638
 Cys Gln Arg Lys Thr Ala Pro Tyr Lys Asn Val Asn Val Gln Asn Phe
 175 180 185

cac atc agc tgg aag gat ggt ctt gcc ttc aat gcc ctg atc cac cgg 686
 His Ile Ser Trp Lys Asp Gly Leu Ala Phe Asn Ala Leu Ile His Arg
 190 195 200
 cac aga cca gag ctg att gag tat gac aag ctg agg aag gac gac cct 734
 His Arg Pro Glu Leu Ile Glu Tyr Asp Lys Leu Arg Lys Asp Asp Pro
 205 210 215
 gtc acc aac ctg aac aat gcc ttc gaa gtg gct gag aaa tac ctc gac 782
 Val Thr Asn Leu Asn Asn Ala Phe Glu Val Ala Glu Lys Tyr Leu Asp
 220 225 230 235
 atc ccc aag atg ctg gat gca gag gac atc glg aac acg gcc cgg ccc 830
 Ile Pro Lys Met Leu Asp Ala Glu Asp Ile Val Asn Thr Ala Arg Pro
 240 245 250
 gac gag aag gcc ata atg acc tat gtg tcc agc ttc tac cat gcc ttt 878
 Asp Glu Lys Ala Ile Met Thr Tyr Val Ser Ser Phe Tyr His Ala Phe
 255 260 265
 tca gga gcg cag aag gct gaa act gaa act gcc gcc aac cgg atc tgt 926
 Ser Gly Ala Gln Lys Ala Glu Thr Glu Thr Ala Ala Asn Arg Ile Cys
 270 275 280
 aag gtg ctg gct gtc aac caa gag aac tgc agc acc tgc atg gag gac 974
 Lys Val Leu Ala Val Asn Gln Glu Asn Cys Ser Thr Ser Met Glu Asp
 285 290 295
 tac gag aag ctg gcc agc gac ctc ctg gag tgg atc cgg cgc acc atc 1022
 Tyr Glu Lys Leu Ala Ser Asp Leu Leu Glu Trp Ile Arg Arg Thr Ile
 300 305 310 315
 ccc tgg ctg gag gac cgt gtg ccc caa aag act atc cag gag atg cag 1070
 Pro Trp Leu Glu Asp Arg Val Pro Gln Lys Thr Ile Gln Glu Met Gln

320	325	330	
cag aag ctg gag gac ttc cgc gac tac cgg cgt gtg cac aag ccg ccc			1118
Gln Lys Leu Glu Asp Phe Arg Asp Tyr Arg Arg Val His Lys Pro Pro			
335	340	345	
aag gtg cag gag aag tgc cag ctg gag atc aac ttc aac agc gtg cag			1166
Lys Val Gln Glu Lys Cys Gln Leu Glu Ile Asn Phe Asn Ser Val Gln			
350	355	360	
acc aag ctg cgc ctc agc aac cgg ccc gcc ttc atg ccc tcc gag ggc			1214
Thr Lys Leu Arg Leu Ser Asn Arg Pro Ala Phe Met Pro Ser Glu Gly			
365	370	375	
aag atg gtc tcg gac atc aac aat ggc tgg cag cac ttg gag cag gct			1262
Lys Met Val Ser Asp Ile Asn Asn Gly Trp Gln His Leu Glu Gln Ala			
380	385	390	395
gag aag ggc tac gag gag tgg ctg ctg aat gag att cgc agg ctg gag			1310
Glu Lys Gly Tyr Glu Glu Trp Leu Leu Asn Glu Ile Arg Arg Leu Glu			
400	405	410	
cgg ctc gac cac ctg gca gag aag ttc cgg cag aaa gcc tcc atc cac			1358
Arg Leu Asp His Leu Ala Glu Lys Phe Arg Gln Lys Ala Ser Ile His			
415	420	425	
gag gcc tgg act gac ggg aag gaa gcc atg ctg aag cac cgg gac tac			1406
Glu Ala Trp Thr Asp Gly Lys Glu Ala Met Leu Lys His Arg Asp Tyr			
430	435	440	
gag acg gcc aca cta tcg gac atc aaa gcc ctc att cgc aag cac gag			1454
Glu Thr Ala Thr Leu Ser Asp Ile Lys Ala Leu Ile Arg Lys His Glu			
445	450	455	
gcc ttc gag agc gac ctg gct gcg cac cag gac cgc gtg gag cag atc			1502
Ala Phe Glu Ser Asp Leu Ala Ala His Gln Asp Arg Val Glu Gln Ile			

460	465	470	475	
gcc gcc tcc gcc cag gag ctc aac gag ctg gai tac tac gac tcc cac				1550
Ala Ala Ser Ala Gln Glu Leu Asn Glu Leu Asp Tyr Tyr Asp Ser His				
	480	485	490	
aat gtc aac acc cgg tgc cag aag atc tgt gac cag tgg gac gcc ctc				1598
Asn Val Asn Thr Arg Cys Gln Lys Ile Cys Asp Gln Trp Asp Ala Leu				
	495	500	505	
ggc tct ctg aca cat agt cgc agg gaa gcc ctg gag aaa aca gag aag				1646
Gly Ser Leu Thr His Ser Arg Arg Glu Ala Leu Glu Lys Thr Glu Lys				
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cag ctg gag gcc atc atc gac cag ctg cac ctg gaa tac gcc aag ccc				1694
Gln Leu Glu Ala Ile Ile Asp Gln Leu His Leu Glu Tyr Ala Lys Pro				
	525	530	535	
gcg gcc ccc ttc aac aac tgg atg gag agc gcc atg gag gac ctc cag				1742
Ala Ala Pro Phe Asn Asn Trp Met Glu Ser Ala Met Glu Asp Leu Gln				
540	545	550	555	
gac atg ttc atc gtc cat acc atc gag gag att gag ggc ctg atc tca				1790
Asp Met Phe Ile Val His Thr Ile Glu Glu Ile Glu Gly Leu Ile Ser				
	560	565	570	
gcc cat gac cag ttc aag tcc acc ctg ccg gac gcc gat agg gag cgc				1838
Ala His Asp Gln Phe Lys Ser Thr Leu Pro Asp Ala Asp Arg Glu Arg				
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gag gcc atc ctg cat cca caa gga ggc cag agg atc gct gag agc aac				1886
Glu Ala Ile Leu His Pro Gln Gly Gly Gln Arg Ile Ala Glu Ser Asn				
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cac atc aag ctg tcg ggc agc aac ccc tac acc acc gtc acc ccg caa				1934

His Ile Lys Leu Ser Gly Ser Asn Pro Tyr Thr Thr Val Thr Pro Gln
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 atc atc aac tcc aag tgg gag aag gtg cag cag ctg gtg cca aaa cgg 1982
 Ile Ile Asn Ser Lys Trp Glu Lys Val Gln Gln Leu Val Pro Lys Arg
 620 625 630 635
 gac cat gcc ctc ctg gag gag cag agc aag cag cag cag tcc aac gag 2030
 Asp His Ala Leu Leu Glu Glu Gln Ser Lys Gln Gln Gln Ser Asn Glu
 640 645 650
 cac ctg cgc cgc cag ttc gcc agc cag gcc aat gtt gtg ggg ccc tgg 2078
 His Leu Arg Arg Gln Phe Ala Ser Gln Ala Asn Val Val Gly Pro Trp
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 atc cag acc aag atg gag gag atc gcg atc tcc att gag atg aac ggg 2126
 Ile Gln Thr Lys Met Glu Glu Ile Ala Ile Ser Ile Glu Met Asn Gly
 670 675 680
 acc ctg gag gac cag ctg agc cac ctg aag cag tat gaa cgc agc atc 2174
 Thr Leu Glu Asp Gln Leu Ser His Leu Lys Gln Tyr Glu Arg Ser Ile
 685 690 695
 gtg gac tac aag ccc aac ctg gac ctg ctg gag cag cag cac cag ctc 2222
 Val Asp Tyr Lys Pro Asn Leu Asp Leu Leu Glu Gln Gln His Gln Leu
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 atc cag gag gcc ctc atc ttc gac aac aag cac acc aac tat acc atg 2270
 Ile Gln Glu Ala Leu Ile Phe Asp Asn Lys His Thr Asn Tyr Thr Met
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 gag cac atc cgc gtg ggc tgg gag cag ctg ctc acc acc att gcc cgc 2318
 Glu His Ile Arg Val Gly Trp Glu Gln Leu Leu Thr Thr Ile Ala Arg
 735 740 745
 acc atc aac gag gtg gag aac cag atc ctt acc cgc gac gcc aag ggc 2366

Thr Ile Asn Glu Val Glu Asn Gln Ile Leu Thr Arg Asp Ala Lys Gly
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 Ile Ser Gln Glu Gln Met Gln Glu Phe Arg Ala Ser Phe Asn His Phe
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 Asp Lys Asp His Gly Gly Ala Leu Gly Arg Gly Val Gln Gly Leu Pro
 780 785 790 795
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 His Gln Pro Gly Leu Arg Arg Gly Glu Arg Pro Ala Gly Glu Ala Glu
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 Phe Asn Arg Ile Met Ser Leu Val Asp Pro Asn His Ser Gly Leu Val
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 acc ttc caa gcc ttc atc gac ttc atg tgg cgg gag acc acc gac acc 2606
 Thr Phe Gln Ala Phe Ile Asp Phe Met Ser Arg Glu Thr Thr Asp Thr
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 Asp Thr Ala Asp Gln Val Ile Thr Ser Phe Lys Val Leu Ala Gly Asp
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 Lys Asn Phe Ile Thr Ala Glu Glu Leu Arg Arg Glu Leu Pro Pro Asp
 860 865 870 875
 cag gcc gag tac tgc atc gcc cgc atg gcg cca tac cag ggc cct gac 2750
 Gln Ala Glu Tyr Cys Ile Ala Arg Met Ala Pro Tyr Gln Gly Pro Asp
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ggc gtg cgc ggt gcc ctc gac tac aag tcc ttc tcc acg gcc ttg tat 2798

Gly Val Arg Gly Ala Leu Asp Tyr Lys Ser Phe Ser Thr Ala Leu Tyr

895

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905

ggc gag agc gac ctg tgaggcccca gagacctgac ccaacacccc cgacgccctc 2853

Gly Glu Ser Asp Leu

910

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 Lys Gln Gln Arg Lys Thr Phe Thr Ala Trp Ser Asn Ser His Leu Arg
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 Lys Ala Gly Thr Gln Ile Glu Asn Ile Asp Glu Asp Phe Arg Asp Gly
 65 70 75 80
 Leu Lys Leu Met Leu Leu Leu Glu Val Ile Ser Gly Glu Arg Leu Pro
 85 90 95
 Lys Pro Glu Arg Gly Lys Met Arg Val His Lys Ile Asn Asn Val Asn
 100 105 110
 Lys Ala Leu Asp Phe Ile Ala Ser Lys Gly Ile Lys Leu Asp Phe His
 115 120 125
 Arg Ala Glu Glu Ile Val Asp Gly Asn Ala Lys Met Thr Leu Gly Met
 130 135 140
 Ile Trp Thr Ile Ile Leu Arg Phe Ala Ile Gln Asp Ile Ser Val Glu
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 Glu Thr Ser Ala Lys Glu Gly Leu Leu Leu Trp Cys Gln Arg Lys Thr
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 Ala Pro Tyr Lys Asn Val Asn Val Gln Asn Phe His Ile Ser Trp Lys
 180 185 190
 Asp Gly Leu Ala Phe Asn Ala Leu Ile His Arg His Arg Pro Glu Leu
 195 200 205
 Ile Glu Tyr Asp Lys Leu Arg Lys Asp Asp Pro Val Thr Asn Leu Asn
 210 215 220
 Asn Ala Phe Glu Val Ala Glu Lys Tyr Leu Asp Ile Pro Lys Met Leu
 225 230 235 240
 Asp Ala Glu Asp Ile Val Asn Thr Ala Arg Pro Asp Glu Lys Ala Ile

245 250 255
Met Thr Tyr Val Ser Ser Phe Tyr His Ala Phe Ser Gly Ala Gln Lys
260 265 270
Ala Glu Thr Glu Thr Ala Ala Asn Arg Ile Cys Lys Val Leu Ala Val
275 280 285
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Ser Asp Leu Leu Glu Trp Ile Arg Arg Thr Ile Pro Trp Leu Glu Asp
305 310 315 320
Arg Val Pro Gln Lys Thr Ile Gln Glu Met Gln Gln Lys Leu Glu Asp
325 330 335
Phe Arg Asp Tyr Arg Arg Val His Lys Pro Pro Lys Val Gln Glu Lys
340 345 350
Cys Gln Leu Glu Ile Asn Phe Asn Ser Val Gln Thr Lys Leu Arg Leu
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Ser Asn Arg Pro Ala Phe Met Pro Ser Glu Gly Lys Met Val Ser Asp
370 375 380
Ile Asn Asn Gly Trp Gln His Leu Glu Gln Ala Glu Lys Gly Tyr Glu
385 390 395 400
Glu Trp Leu Leu Asn Glu Ile Arg Arg Leu Glu Arg Leu Asp His Leu
405 410 415
Ala Glu Lys Phe Arg Gln Lys Ala Ser Ile His Glu Ala Trp Thr Asp
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435 440 445
Ser Asp Ile Lys Ala Leu Ile Arg Lys His Glu Ala Phe Glu Ser Asp

WO 01/25427

PCT/JP00/06840

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Leu Ala Ala His Gln Asp Arg Val Glu Gln Ile Ala Ala Ser Ala Gln

455

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Glu Leu Asn Glu Leu Asp Tyr Tyr Asp Ser His Asn Val Asn Thr Arg

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475

495

485

490

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Cys Gln Lys Ile Cys Asp Gln Trp Asp Ala Leu Gly Ser Leu Thr His

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Ser Arg Arg Glu Ala Leu Glu Lys Thr Glu Lys Gln Leu Glu Ala Ile

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Ile Asp Gln Leu His Leu Glu Tyr Ala Lys Pro Ala Ala Pro Phe Asn

530

535

560

Asn Trp Met Glu Ser Ala Met Glu Asp Leu Gln Asp Met Phe Ile Val

545

550

575

His Thr Ile Glu Glu Ile Glu Gly Leu Ile Ser Ala His Asp Gln Phe

565

590

Lys Ser Thr Leu Pro Asp Ala Asp Arg Glu Arg Glu Ala Ile Leu His

580

605

Pro Gln Gly Gly Gln Arg Ile Ala Glu Ser Asn His Ile Lys Leu Ser

595

620

Gly Ser Asn Pro Tyr Thr Thr Val Thr Pro Gln Ile Ile Asn Ser Lys

610

640

Trp Glu Lys Val Gln Gln Leu Val Pro Lys Arg Asp His Ala Leu Leu

625

655

Glu Glu Gln Ser Lys Gln Gln Gln Ser Asn Glu His Leu Arg Arg Gln

645

665

Phe Ala Ser Gln Ala Asn Val Val Gly Pro Trp Ile Gln Thr Lys Met

660

163/527

WO 01/25427

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 675 680 685
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 690 695 700
 Asn Leu Asp Leu Leu Glu Gln Gln His Gln Leu Ile Gln Glu Ala Leu
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 Ile Phe Asp Asn Lys His Thr Asn Tyr Thr Met Glu His Ile Arg Val
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 Gly Trp Glu Gln Leu Leu Thr Thr Ile Ala Arg Thr Ile Asn Glu Val
 740 745 750
 Glu Asn Gln Ile Leu Thr Arg Asp Ala Lys Gly Ile Ser Gln Glu Gln
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 Met Gln Glu Phe Arg Ala Ser Phe Asn His Phe Asp Lys Asp His Gly
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Asn Thr Phe Thr Arg Trp Cys Asn Glu His Leu Lys Cys Val Gly Lys

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cgc ctg acc gac ctg cag cgc gac ctc agc gac ggg ctc cgg ctc atc 262

Arg Leu Thr Asp Leu Gln Arg Asp Leu Ser Asp Gly Leu Arg Leu Ile

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 Pro Arg Pro Asn Phe Arg Gln Met Lys Leu Glu Asn Val Ser Val Ala
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 Leu Glu Phe Leu Glu Arg Glu His Ile Lys Leu Val Ser Ile Asp Ser
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 Thr Leu Ile Leu His Tyr Ser Ile Ser Met Pro Met Trp Glu Asp Glu
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 Asp Asp Glu Asp Ala Arg Lys Gln Thr Pro Lys Gln Arg Leu Leu Gly
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 Trp Ile Gln Asn Lys Val Pro Gln Leu Pro Ile Thr Asn Phe Asn Arg
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 ccc ggt ctc tgc ccc gac tgg gag gcc tgg gat ccc aac cag ccc gtg 694
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Glu Asn Ser Arg Glu Ala Met Gln Gln Ala Asp Asp Trp Leu Gly Val
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 ccc cag gtc att gcc cct gag gag att gtg gac ccc aac gtg gat gag 790
 Pro Gln Val Ile Ala Pro Glu Glu Ile Val Asp Pro Asn Val Asp Glu
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 His Ser Val Met Thr Tyr Leu Ser Gln Phe Pro Lys Ala Lys Leu Lys
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cgc tac acc atc atg gtg ctg ttt gcc aac cag gag atc ccc gcc agc			2614
Arg Tyr Thr Ile Met Val Leu Phe Ala Asn Gln Glu Ile Pro Ala Ser			
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ccc ttc cac atc aag gtg gac cca tcc cac gat gcc agc aaa gtc aag			2662
Pro Phe His Ile Lys Val Asp Pro Ser His Asp Ala Ser Lys Val Lys			
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 920 925 930
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 Glu Glu Gly Pro Tyr Lys Val Asp Ile Thr Tyr Asp Gly His Pro Val
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Lys Val Cys Ala Tyr Gly Pro Gly Leu Lys Gly Gly Leu Val Gly Thr
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 Asn Gly Asp Gly Ser Cys Ala Val Ser Tyr Leu Pro Thr Glu Pro Gly
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 gag tac acc atc aac atc ctg ttt gct gag gcc cac atc cct ggc tgc 3478
 Glu Tyr Thr Ile Asn Ile Leu Phe Ala Glu Ala His Ile Pro Gly Ser
 1110 1115 1120
 ccc ttc aaa gcc acc att cgg cct gtg ttt gac ccg agc aag gtg cgg 3526
 Pro Phe Lys Ala Thr Ile Arg Pro Val Phe Asp Pro Ser Lys Val Arg
 1125 1130 1135
 gcc agt gga ccg ggc ctg gag cgc ggc aag gtc ggt gag gca gcc acc 3574
 Ala Ser Gly Pro Gly Leu Glu Arg Gly Lys Val Gly Glu Ala Ala Thr
 1140 1145 1150 1155
 ttc act gtg gac tgc tca gag gca ggc gag gcg gag ctg acc att gag 3622
 Phe Thr Val Asp Cys Ser Glu Ala Gly Glu Ala Glu Leu Thr Ile Glu
 1160 1165 1170
 atc ctg tgc gat gcc ggg gtc aag gcc gag gtg ctg atc cac aac aac 3670
 Ile Leu Ser Asp Ala Gly Val Lys Ala Glu Val Leu Ile His Asn Asn
 1175 1180 1185

gcg gat ggc acc tac cac atc acc tac agc cct gcc ttc cct ggc acc 3718
 Ala Asp Gly Thr Tyr His Ile Thr Tyr Ser Pro Ala Phe Pro Gly Thr
 1190 1195 1200
 tac acc att acc atc aag tat ggc ggg cat ccc gtg ccc aaa ttc ccc 3766
 Tyr Thr Ile Thr Ile Lys Tyr Gly Gly His Pro Val Pro Lys Phe Pro
 1205 1210 1215
 acc cgt gtc cat gtg cag cct gcg gtc gat acc agt ggc gtc aag gtc 3814
 Thr Arg Val His Val Gln Pro Ala Val Asp Thr Ser Gly Val Lys Val
 1220 1225 1230 1235
 tca ggg cct ggt gtl gag cca cac ggt gtc ctg cgg gag gtg acc act 3862
 Ser Gly Pro Gly Val Glu Pro His Gly Val Leu Arg Glu Val Thr Thr
 1240 1245 1250
 gag ttc act gtg gat gca aga tcc cta aca gcc aca ggc ggc aac cac 3910
 Glu Phe Thr Val Asp Ala Arg Ser Leu Thr Ala Thr Gly Gly Asn His
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 gtg acg gct cgt gtg ctc aac ccc tcg ggg gcc aag aca gac acc tat 3958
 Val Thr Ala Arg Val Leu Asn Pro Ser Gly Ala Lys Thr Asp Thr Tyr
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 gtg aca gac aat ggg gac ggc acc tac cga gtg cag tac acc gcc tac 4006
 Val Thr Asp Asn Gly Asp Gly Thr Tyr Arg Val Gln Tyr Thr Ala Tyr
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 gag gag ggc gtg cat ctg gtg gag gtc ctg tat gat gag gtc gct gtg 4054
 Glu Glu Gly Val His Leu Val Glu Val Leu Tyr Asp Glu Val Ala Val
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 ccc aag agc ccc ttc cga gtg ggc gtg acc gag ggc tgt gat ccc acc 4102
 Pro Lys Ser Pro Phe Arg Val Gly Val Thr Glu Gly Cys Asp Pro Thr
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cgc gtc cga gcc ttc ggg cca ggc ctg gag ggt ggc ttg gtc aac aag 4150
 Arg Val Arg Ala Phe Gly Pro Gly Leu Glu Gly Gly Leu Val Asn Lys
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 Gly Leu Ala Ile Glu Gly Pro Ser Glu Ala Lys Met Ser Cys Lys Asp
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 Asn Lys Asp Gly Ser Cys Thr Val Glu Tyr Ile Pro Phe Thr Pro Gly
 1380 1385 1390 1395
 gac tat gac gtc aac atc acc ttc ggg ggg cgg ccc atc cca ggg agc 4342
 Asp Tyr Asp Val Asn Ile Thr Phe Gly Gly Arg Pro Ile Pro Gly Ser
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 ccg ttc cgc gtg cca gtg aag gat gtg gtg gac cct ggg aag gtg aag 4390
 Pro Phe Arg Val Pro Val Lys Asp Val Val Asp Pro Gly Lys Val Lys
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 tgc tca ggg cca ggg ctg ggg gct ggt gtc agg gcc cgg gtt cct cag 4438
 Cys Ser Gly Pro Gly Leu Gly Ala Gly Val Arg Ala Arg Val Pro Gln
 1430 1435 1440
 acc ttc aca gtg gac tgc agt caa gct ggc cgg gcg ccc ctg cag gtg 4486
 Thr Phe Thr Val Asp Cys Ser Gln Ala Gly Arg Ala Pro Leu Gln Val
 1445 1450 1455
 gct gtg ctg ggc ccc aca ggt gtg gcc gag cct gtg gag gtg cgg gac 4534
 Ala Val Leu Gly Pro Thr Gly Val Ala Glu Pro Val Glu Val Arg Asp

1460	1465	1470	1475	
aat gga gat ggc acc cac act gtc cac tac acc cca gcc act gac ggg				4582
Asn Gly Asp Gly Thr His Thr Val His Tyr Thr Pro Ala Thr Asp Gly				
	1480	1485	1490	
ccc tac acg gta gcc gtc aag tat gct gac cag gag gtg cca cgc agc				4630
Pro Tyr Thr Val Ala Val Lys Tyr Ala Asp Gln Glu Val Pro Arg Ser				
	1495	1500	1505	
ccc ttc aag atc aag gtc ctc cca gct cat gat gcc agc aag gtg cgg				4678
Pro Phe Lys Ile Lys Val Leu Pro Ala His Asp Ala Ser Lys Val Arg				
	1510	1515	1520	
gcc agc ggg cca ggc ctc aac gcc tct ggc atc cct gcc agc ctg cct				4726
Ala Ser Gly Pro Gly Leu Asn Ala Ser Gly Ile Pro Ala Ser Leu Pro				
	1525	1530	1535	
gtg gag ttc acc atc gac gca cgg gac gcg ggc gag ggg ttg ctc act				4774
Val Glu Phe Thr Ile Asp Ala Arg Asp Ala Gly Glu Gly Leu Leu Thr				
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gtc cag atc ttg ggc ccc gag ggt aag ccc aag aag gcc aac atc cgg				4822
Val Gln Ile Leu Gly Pro Glu Gly Lys Pro Lys Lys Ala Asn Ile Arg				
	1560	1565	1570	
gac aat ggg gat ggc acg tac gct gtg tcc tac ctg ccg gac atg agt				4870
Asp Asn Gly Asp Gly Thr Tyr Ala Val Ser Tyr Leu Pro Asp Met Ser				
	1575	1580	1585	
ggc cgg tac acc atc acc atc aag tat ggc ggt gat gag atc ccc tac				4918
Gly Arg Tyr Thr Ile Thr Ile Lys Tyr Gly Gly Asp Glu Ile Pro Tyr				
	1590	1595	1600	
tcg ccc ttc cgc atc cat gct ctg ccc act ggg gat gcc agc aag tgc				4966
Ser Pro Phe Arg Ile His Ala Leu Pro Thr Gly Asp Ala Ser Lys Cys				

1605	1610	1615	
ctc gtc aca gtg tcc att gga ggc cat ggc ctg ggt gcc tgc ctg ggc	5014		
Leu Val Thr Val Ser Ile Gly Gly His Gly Leu Gly Ala Cys Leu Gly			
1620	1625	1630	1635
cct cga atc cag att ggg cag gag acg gtg atc acg gtg gat gcc aag	5062		
Pro Arg Ile Gln Ile Gly Gln Glu Thr Val Ile Thr Val Asp Ala Lys			
1640	1645	1650	
gca gcc ggt gag ggg aag gtg aca tgc acg gtg tcc acg ccg gat ggc	5110		
Ala Ala Gly Glu Gly Lys Val Thr Cys Thr Val Ser Thr Pro Asp Gly			
1655	1660	1665	
gca gag ctc gat gtg gat gtg gtt gag aac cat gac ggt acc ttt gac	5158		
Ala Glu Leu Asp Val Asp Val Val Glu Asn His Asp Gly Thr Phe Asp			
1670	1675	1680	
atc tac tac aca gcg ccc gag ccg ggc aag tac gtc atc acc atc cgc	5206		
Ile Tyr Tyr Thr Ala Pro Glu Pro Gly Lys Tyr Val Ile Thr Ile Arg			
1685	1690	1695	
ttc ggg ggt gag cac atc ccc aac agc ccc ttc cac gtg ctg gcg tgt	5254		
Phe Gly Gly Glu His Ile Pro Asn Ser Pro Phe His Val Leu Ala Cys			
1700	1705	1710	1715
gac ccc ctg ccg cac gag gag gag ccc tct gaa gtg cca cag ctg cgc	5302		
Asp Pro Leu Pro His Glu Glu Glu Pro Ser Glu Val Pro Gln Leu Arg			
1720	1725	1730	
cag ccc tac gct cct ccc cgg ccc ggc gcc cgc ccc aca cac tgg gcc	5350		
Gln Pro Tyr Ala Pro Pro Arg Pro Gly Ala Arg Pro Thr His Trp Ala			
1735	1740	1745	
aca gag gag cca gtg gtg cct gtg gag cca atg gag tcc atg ctg agg	5398		

Thr Glu Glu Pro Val Val Pro Val Glu Pro Met Glu Ser Met Leu Arg
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 Pro Phe Asn Leu Val Ile Pro Phe Ala Val Gln Lys Gly Glu Leu Thr
 1765 1770 1775
 gga gag gtg cgg atg ccc tcg ggg aag acg gca cgg ccc aac atc acc 5494
 Gly Glu Val Arg Met Pro Ser Gly Lys Thr Ala Arg Pro Asn Ile Thr
 1780 1785 1790 1795
 gac aac aag gac ggc acc atc acg gtg agg tat gca ccc act gag aaa 5542
 Asp Asn Lys Asp Gly Thr Ile Thr Val Arg Tyr Ala Pro Thr Glu Lys
 1800 1805 1810
 ggc ctg cac cag atg ggg atc aag tat gac ggc aac cac atc cct ggg 5590
 Gly Leu His Gln Met Gly Ile Lys Tyr Asp Gly Asn His Ile Pro Gly
 1815 1820 1825
 agc ccc tta cag ttc tat gtg gat gcc atc aac agc cgc cat gtc agt 5638
 Ser Pro Leu Gln Phe Tyr Val Asp Ala Ile Asn Ser Arg His Val Ser
 1830 1835 1840
 gcc tat ggg cca ggc ctg agc cat ggc atg gtc aac aag cca gcc acc 5686
 Ala Tyr Gly Pro Gly Leu Ser His Gly Met Val Asn Lys Pro Ala Thr
 1845 1850 1855
 ttc act att gtc acc aaa gat gct gga gaa ggg ggt ctg tca ctg gcc 5734
 Phe Thr Ile Val Thr Lys Asp Ala Gly Glu Gly Gly Leu Ser Leu Ala
 1860 1865 1870 1875
 gtg gag ggc cca tcc aag gca gag atc acc tgt aag gac aac aag gat 5782
 Val Glu Gly Pro Ser Lys Ala Glu Ile Thr Cys Lys Asp Asn Lys Asp
 1880 1885 1890
 ggc acc tgc acc gtg tcc tat ctg ccg act gcg cct gga gac tac agc 5830

Gly Thr Cys Thr Val Ser Tyr Leu Pro Thr Ala Pro Gly Asp Tyr Ser
 1895 1900 1905
 atc atc gtg cgc ttc gat gac aag cac atc ccg ggg agc ccc ttc aca 5878
 Ile Ile Val Arg Phe Asp Asp Lys His Ile Pro Gly Ser Pro Phe Thr
 1910 1915 1920
 gcc aag atc aca ggt gat gac tcc atg agg acc tca cag ctg aat gtg 5926
 Ala Lys Ile Thr Gly Asp Asp Ser Met Arg Thr Ser Gln Leu Asn Val
 1925 1930 1935
 ggc acc tcc acg gac gtg tca ctg aag atc acc gag agt gat ctg agc 5974
 Gly Thr Ser Thr Asp Val Ser Leu Lys Ile Thr Glu Ser Asp Leu Ser
 1940 1945 1950 1955
 cag ctg acc gcc agc atc cgt gcc ccc tcc ggc aac gag gag ccc tgc 6022
 Gln Leu Thr Ala Ser Ile Arg Ala Pro Ser Gly Asn Glu Glu Pro Cys
 1960 1965 1970
 ctg ctg aag cgc ctg ccc aac cgg cac att ggg atc tcc ttc acc ccc 6070
 Leu Leu Lys Arg Leu Pro Asn Arg His Ile Gly Ile Ser Phe Thr Pro
 1975 1980 1985
 aag gag gtc ggg gag cac gtg gtg agc gtg cgc aag agt ggc aag cat 6118
 Lys Glu Val Gly Glu His Val Val Ser Val Arg Lys Ser Gly Lys His
 1990 1995 2000
 gtc acc aac agc ccc ttc aag atc ctg gtg ggg cca tct gag atc ggg 6166
 Val Thr Asn Ser Pro Phe Lys Ile Leu Val Gly Pro Ser Glu Ile Gly
 2005 2010 2015
 gac gcc agc aag gtg cgg gtc tgg ggc aag ggg ctt tcc gag gga cac 6214
 Asp Ala Ser Lys Val Arg Val Trp Gly Lys Gly Leu Ser Glu Gly His
 2020 2025 2030 2035

aca ttc cag gtg gca gag ttc atc gtg gac act cgc aat gca ggt tat 6262
 Thr Phe Gln Val Ala Glu Phe Ile Val Asp Thr Arg Asn Ala Gly Tyr
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 Gly Gly Leu Gly Leu Ser Ile Glu Gly Pro Ser Lys Val Asp Ile Asn
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 Cys Glu Asp Met Glu Asp Gly Thr Cys Lys Val Thr Tyr Cys Pro Thr
 2070 2075 2080
 gag ccc ggc acc tac atc atc aac atc aag ttt gct gac aag cac glg 6406
 Glu Pro Gly Thr Tyr Ile Ile Asn Ile Lys Phe Ala Asp Lys His Val
 2085 2090 2095
 cct gga agc ccc ttc act gtg aag gtg acc ggc gag ggc cgc atg aag 6454
 Pro Gly Ser Pro Phe Thr Val Lys Val Thr Gly Glu Gly Arg Met Lys
 2100 2105 2110 2115
 gag agc atc acc cgg cgg aga cag gca cct tcc atc gcc acc atc ggc 6502
 Glu Ser Ile Thr Arg Arg Arg Gln Ala Pro Ser Ile Ala Thr Ile Gly
 2120 2125 2130
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 Ser Thr Cys Asp Leu Asn Leu Lys Ile Pro Gly Asn Trp Phe Gln Met
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 Val Ser Ala Gln Glu Arg Leu Thr Arg Thr Phe Thr Arg Ser Ser His
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 acc tac acc cgc acg gag cgc acg gag atc agc aag acg cgg ggc ggg 6646
 Thr Tyr Thr Arg Thr Glu Arg Thr Glu Ile Ser Lys Thr Arg Gly Gly
 2165 2170 2175

gag aca aag ccc gag gtg cgg gtg gag gag tcc acc cag gtc ggc ggg 6694
 Glu Thr Lys Pro Glu Val Arg Val Glu Glu Ser Thr Gln Val Gly Gly
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 Asp Pro Phe Pro Ala Val Phe Gly Asp Phe Leu Gly Arg Glu Arg Leu
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 Gly Ser Phe Gly Ser Ile Thr Arg Gln Gln Glu Gly Glu Ala Ser Ser
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 Gln Asp Met Thr Ala Gln Val Thr Ser Pro Ser Gly Lys Val Glu Ala
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 Ala Glu Ile Val Glu Gly Glu Asp Ser Ala Tyr Ser Val Arg Phe Val
 2245 2250 2255
 ccc cag gaa atg ggg ccc cat acg gtc gct gtc aag tac cgt ggc cag 6934
 Pro Gln Glu Met Gly Pro His Thr Val Ala Val Lys Tyr Arg Gly Gln
 2260 2265 2270 2275
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 His Val Pro Gly Ser Pro Phe Gln Phe Thr Val Gly Pro Leu Gly Glu
 2280 2285 2290
 ggt ggt gcc cac aag gtg cgg gcc gga cga gca ggg ctg gag cga ggt 7030
 Gly Gly Ala His Lys Val Arg Ala Gly Arg Ala Gly Leu Glu Arg Gly
 2295 2300 2305
 gtg gcc ggc gtg cca gcc gag ttc agc atc tgg acc cgg gag gct ggc 7078
 Val Ala Gly Val Pro Ala Glu Phe Ser Ile Trp Thr Arg Glu Ala Gly

2310	2315	2320	
gct ggg ggc ctg tcc att gct gtc gag ggt cct agc aaa gcg gag att			7126
Ala Gly Gly Leu Ser Ile Ala Val Glu Gly Pro Ser Lys Ala Glu Ile			
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gca ttt gag gat cgc aaa gat ggc tcc tgc ggc gtc tcc tat gtc gtc			7174
Ala Phe Glu Asp Arg Lys Asp Gly Ser Cys Gly Val Ser Tyr Val Val			
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cag gaa cca ggt gac tat gag gtc tcc atc aag ttc aat gat gag cac			7222
Gln Glu Pro Gly Asp Tyr Glu Val Ser Ile Lys Phe Asn Asp Glu His			
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Ile Pro Asp Ser Pro Phe Val Val Pro Val Ala Ser Leu Ser Asp Asp			
2375	2380	2385	
gct cgc cgt ctc act gtc acc agc ctc cag gag acg ggg ctc aag gtg			7318
Ala Arg Arg Leu Thr Val Thr Ser Leu Gln Glu Thr Gly Leu Lys Val			
2390	2395	2400	
aac cag cca gcg tcc ttt gcc gtg cag ctg aac ggt gcc cgg ggc gtg			7366
Asn Gln Pro Ala Ser Phe Ala Val Gln Leu Asn Gly Ala Arg Gly Val			
2405	2410	2415	
att gat gcc cgg gtc cac aca ccc tcg ggg gct gtg gag gag tgc tac			7414
Ile Asp Ala Arg Val His Thr Pro Ser Gly Ala Val Glu Glu Cys Tyr			
2420	2425	2430	2435
gtc tct gag ctg gac agt gac aag cac acc atc cgc ttc atc ccc cac			7462
Val Ser Glu Leu Asp Ser Asp Lys His Thr Ile Arg Phe Ile Pro His			
2440	2445	2450	
gag aat ggc gtc cac tcc atc gat gtc aag ttc aac ggt gcc cac atc			7510
Glu Asn Gly Val His Ser Ile Asp Val Lys Phe Asn Gly Ala His Ile			

2455	2460	2465	
cct gga agt ccc ttc aag atc cgc gtt ggg gag cag agc cag gct ggg	7558		
Pro Gly Ser Pro Phe Lys Ile Arg Val Gly Glu Gln Ser Gln Ala Gly			
2470	2475	2480	
gac cca ggc ttg gtg tca gcc tac ggt cct ggg ctc gag gga ggc act	7606		
Asp Pro Gly Leu Val Ser Ala Tyr Gly Pro Gly Leu Glu Gly Gly Thr			
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acc ggt gtg tca tca gag ttc atc gtg aac acc ctg aat gcc ggc tcg	7654		
Thr Gly Val Ser Ser Glu Phe Ile Val Asn Thr Leu Asn Ala Gly Ser			
2500	2505	2510	2515
ggg gcc ttg tct gtc acc att gat ggc ccc tcc aag gtg cag ctg gac	7702		
Gly Ala Leu Ser Val Thr Ile Asp Gly Pro Ser Lys Val Gln Leu Asp			
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Cys Arg Glu Cys Pro Glu Gly His Val Val Thr Tyr Thr Pro Met Ala			
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Pro Gly Asn Tyr Leu Ile Ala Ile Lys Tyr Gly Gly Pro Gln His Ile			
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Val Gly Ser Pro Phe Lys Ala Lys Val Thr Gly Pro Arg Leu Ser Gly			
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Gly His Ser Leu His Glu Thr Ser Thr Val Leu Val Glu Thr Val Thr			
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Lys Ser Ser Ser Ser Arg Gly Ser Ser Tyr Ser Ser Ile Pro Lys Phe
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 Ser Ser Asp Ala Ser Lys Val Val Thr Arg Gly Pro Gly Leu Ser Gln
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 gcc ttc gtg ggc cag aag aac tcc ttc acc gtg gac tgc agc aaa gca 8038
 Ala Phe Val Gly Gln Lys Asn Ser Phe Thr Val Asp Cys Ser Lys Ala
 2630 2635 2640
 ggc acc aac atg atg atg gtg ggc gtg cac ggc ccc aag acc ccc igt 8086
 Gly Thr Asn Met Met Met Val Gly Val His Gly Pro Lys Thr Pro Cys
 2645 2650 2655
 gag gag gtg tac gtg aag cac atg ggg aac cgg gtg tac aat gtc acc 8134
 Glu Glu Val Tyr Val Lys His Met Gly Asn Arg Val Tyr Asn Val Thr
 2660 2665 2670 2675
 tac act gtc aag gag aaa ggg gac tac atc ctc att gtc aag tgg ggt 8182
 Tyr Thr Val Lys Glu Lys Gly Asp Tyr Ile Leu Ile Val Lys Trp Gly
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<210> 44

<211> 2705

<212> PRT

<213> Homo sapiens

<400> 44

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Ile Gln Gln Asn Thr Phe Thr Arg Trp Cys Asn Glu His Leu Lys Cys

20 25 30

Val Gly Lys Arg Leu Thr Asp Leu Gln Arg Asp Leu Ser Asp Gly Leu

35 40 45

Arg Leu Ile Ala Leu Leu Glu Val Leu Ser Gln Lys Arg Met Tyr Arg

50 55 60

Lys Phe His Pro Arg Pro Asn Phe Arg Gln Met Lys Leu Glu Asn Val

65 70 75 80

Ser Val Ala Leu Glu Phe Leu Glu Arg Glu His Ile Lys Leu Val Ser

85 90 95

Ile Asp Ser Lys Ala Ile Val Asp Gly Asn Leu Lys Leu Ile Leu Gly

100 105 110

Leu Ile Trp Thr Leu Ile Leu His Tyr Ser Ile Ser Met Pro Met Trp

115	120	125	
Glu Asp Glu Asp Asp	Glu Asp Ala Arg Lys	Gln Thr Pro Lys	Gln Arg
130	135	140	
Leu Leu Gly Trp Ile	Gln Asn Lys Val Pro	Gln Leu Pro Ile	Thr Asn
145	150	155	160
Phe Asn Arg Asp Trp	Gln Asp Gly Lys Ala	Leu Gly Ala Leu	Val Asp
165	170	175	
Asn Cys Ala Pro Gly	Leu Cys Pro Asp Trp	Glu Ala Trp Asp	Pro Asn
180	185	190	
Gln Pro Val Glu Asn	Ser Arg Glu Ala Met	Gln Gln Ala Asp	Asp Trp
195	200	205	
Leu Gly Val Pro Gln	Val Ile Ala Pro Glu	Glu Ile Val Asp	Pro Asn
210	215	220	
Val Asp Glu His Ser	Val Met Thr Tyr Leu	Ser Gln Phe Pro	Lys Ala
225	230	235	240
Lys Leu Lys Pro Gly	Ala Pro Val Arg Ser	Lys Gln Leu Asn	Pro Lys
245	250	255	
Lys Ala Ile Ala Tyr	Gly Pro Gly Ile Glu	Pro Gln Gly Asn	Thr Val
260	265	270	
Leu Gln Pro Ala His	Phe Thr Val Gln Thr	Val Asp Ala Gly	Val Gly
275	280	285	
Glu Val Leu Val Tyr	Ile Glu Asp Pro Glu	Gly His Thr Glu	Glu Ala
290	295	300	
Lys Val Val Pro Asn	Asn Asp Lys Asp Arg	Thr Tyr Ala Val	Ser Tyr
305	310	315	320
Val Pro Lys Val Ala	Gly Leu His Lys Val	Thr Val Leu Phe	Ala Gly

325 330 335
Gln Asn Ile Glu Arg Ser Pro Phe Glu Val Asn Val Gly Met Ala Leu
340 345 350
Gly Asp Ala Asn Lys Val Ser Ala Arg Gly Pro Gly Leu Glu Pro Val
355 360 365
Gly Asn Val Ala Asn Lys Pro Thr Tyr Phe Asp Ile Tyr Thr Ala Gly
370 375 380
Ala Gly Thr Gly Asp Val Ala Val Val Ile Val Asp Pro Gln Gly Arg
385 390 395 400
Arg Asp Thr Val Glu Val Ala Leu Glu Asp Lys Gly Asp Ser Thr Phe
405 410 415
Arg Cys Thr Tyr Arg Pro Ala Met Glu Gly Pro His Thr Val His Val
420 425 430
Ala Phe Ala Gly Ala Pro Ile Thr Arg Ser Pro Phe Pro Val His Val
435 440 445
Ser Glu Ala Cys Asn Pro Asn Ala Cys Arg Ala Ser Gly Arg Gly Leu
450 455 460
Gln Pro Lys Gly Val Arg Val Lys Glu Val Ala Asp Phe Lys Val Phe
465 470 475 480
Thr Lys Gly Ala Gly Ser Gly Glu Leu Lys Val Thr Val Lys Gly Pro
485 490 495
Lys Gly Thr Glu Glu Pro Val Lys Val Arg Glu Ala Gly Asp Gly Val
500 505 510
Phe Glu Cys Glu Tyr Tyr Pro Val Val Pro Gly Lys Tyr Val Val Thr
515 520 525
Ile Thr Trp Gly Gly Tyr Ala Ile Pro Arg Ser Pro Phe Glu Val Gln
530 535 540

Val Ser Pro Glu Ala Gly Val Gln Lys Val Arg Ala Trp Gly Pro Gly
 545 550 555 560
 Leu Glu Thr Gly Gln Val Gly Lys Ser Ala Asp Phe Val Val Glu Ala
 565 570 575
 Ile Gly Thr Glu Val Gly Thr Leu Gly Phe Ser Ile Glu Gly Pro Ser
 580 585 590
 Gln Ala Lys Ile Glu Cys Asp Asp Lys Gly Asp Gly Ser Cys Asp Val
 595 600 605
 Arg Tyr Trp Pro Thr Glu Pro Gly Glu Tyr Ala Val His Val Ile Cys
 610 615 620
 Asp Asp Glu Asp Ile Arg Asp Ser Pro Phe Ile Ala His Ile Leu Pro
 625 630 635 640
 Ala Pro Pro Asp Cys Phe Pro Asp Lys Val Lys Ala Phe Gly Pro Gly
 645 650 655
 Leu Glu Pro Thr Gly Cys Ile Val Asp Lys Pro Ala Glu Phe Thr Ile
 660 665 670
 Asp Ala Arg Ala Ala Gly Lys Gly Asp Leu Lys Leu Tyr Ala Gln Asp
 675 680 685
 Ala Asp Gly Cys Pro Ile Asp Ile Lys Val Ile Pro Asn Gly Asn Gly
 690 695 700
 Thr Phe Arg Cys Ser Tyr Val Pro Thr Lys Pro Ile Lys His Thr Ile
 705 710 715 720
 Ile Ile Ser Trp Gly Gly Val Asn Val Pro Lys Ser Pro Phe Arg Val
 725 730 735
 Asn Val Gly Glu Gly Ser His Pro Glu Arg Val Lys Val Tyr Gly Pro
 740 745 750

Gly Val Glu Lys Thr Gly Leu Lys Ala Asn Glu Pro Thr Tyr Phe Thr
755 760 765

Val Asp Cys Ser Glu Ala Gly Gln Gly Asp Val Ser Ile Gly Ile Lys
770 775 780

Cys Ala Pro Gly Val Val Gly Pro Ala Glu Ala Asp Ile Asp Phe Asp
785 790 795 800

Ile Ile Lys Asn Asp Asn Asp Thr Phe Thr Val Lys Tyr Thr Pro Pro
805 810 815

Gly Ala Gly Arg Tyr Thr Ile Met Val Leu Phe Ala Asn Gln Glu Ile
820 825 830

Pro Ala Ser Pro Phe His Ile Lys Val Asp Pro Ser His Asp Ala Ser
835 840 845

Lys Val Lys Ala Glu Gly Pro Gly Leu Asn Arg Thr Gly Val Glu Val
850 855 860

Gly Lys Pro Thr His Phe Thr Val Leu Thr Lys Gly Ala Gly Lys Ala
865 870 875 880

Lys Leu Asp Val Gln Phe Ala Gly Thr Ala Lys Gly Glu Val Val Arg
885 890 895

Asp Phe Glu Ile Ile Asp Asn His Asp Tyr Ser Tyr Thr Val Lys Tyr
900 905 910

Thr Ala Val Gln Gln Gly Asn Met Ala Val Thr Val Thr Tyr Gly Gly
915 920 925

Asp Pro Val Pro Lys Ser Pro Phe Val Val Asn Val Ala Pro Pro Leu
930 935 940

Asp Leu Ser Lys Ile Lys Val Gln Gly Leu Asn Ser Lys Val Ala Val
945 950 955 960

Gly Gln Glu Gln Ala Phe Ser Val Asn Thr Arg Gly Ala Gly Gly Gln

965 970 975
Gly Gln Leu Asp Val Arg Met Thr Ser Pro Ser Arg Arg Pro Ile Pro
980 985 990
Cys Lys Leu Glu Pro Gly Gly Gly Ala Glu Ala Gln Ala Val Arg Tyr
995 1000 1005
Met Pro Pro Glu Glu Gly Pro Tyr Lys Val Asp Ile Thr Tyr Asp Gly
1010 1015 1020
His Pro Val Pro Gly Ser Pro Phe Ala Val Glu Gly Val Leu Pro Pro
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Asp Pro Ser Lys Val Cys Ala Tyr Gly Pro Gly Leu Lys Gly Gly Leu
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Val Gly Thr Pro Ala Pro Phe Ser Ile Asp Thr Lys Gly Ala Gly Thr
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Gly Gly Leu Gly Leu Thr Val Glu Gly Pro Cys Glu Ala Lys Ile Glu
1075 1080 1085
Cys Gln Asp Asn Gly Asp Gly Ser Cys Ala Val Ser Tyr Leu Pro Thr
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Glu Pro Gly Glu Tyr Thr Ile Asn Ile Leu Phe Ala Glu Ala His Ile
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Pro Gly Ser Pro Phe Lys Ala Thr Ile Arg Pro Val Phe Asp Pro Ser
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Lys Val Arg Ala Ser Gly Pro Gly Leu Glu Arg Gly Lys Val Gly Glu
1140 1145 1150
Ala Ala Thr Phe Thr Val Asp Cys Ser Glu Ala Gly Glu Ala Glu Leu
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Thr Ile Glu Ile Leu Ser Asp Ala Gly Val Lys Ala Glu Val Leu Ile

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His Asn Asn Ala Asp Gly Thr Tyr His Ile Thr Tyr Ser Pro Ala Phe			
1185	1190	1195	1200
Pro Gly Thr Tyr Thr Ile Thr Ile Lys Tyr Gly Gly His Pro Val Pro			
	1205	1210	1215
Lys Phe Pro Thr Arg Val His Val Gln Pro Ala Val Asp Thr Ser Gly			
	1220	1225	1230
Val Lys Val Ser Gly Pro Gly Val Glu Pro His Gly Val Leu Arg Glu			
	1235	1240	1245
Val Thr Thr Glu Phe Thr Val Asp Ala Arg Ser Leu Thr Ala Thr Gly			
	1250	1255	1260
Gly Asn His Val Thr Ala Arg Val Leu Asn Pro Ser Gly Ala Lys Thr			
1265	1270	1275	1280
Asp Thr Tyr Val Thr Asp Asn Gly Asp Gly Thr Tyr Arg Val Gln Tyr			
	1285	1290	1295
Thr Ala Tyr Glu Glu Gly Val His Leu Val Glu Val Leu Tyr Asp Glu			
	1300	1305	1310
Val Ala Val Pro Lys Ser Pro Phe Arg Val Gly Val Thr Glu Gly Cys			
	1315	1320	1325
Asp Pro Thr Arg Val Arg Ala Phe Gly Pro Gly Leu Glu Gly Gly Leu			
	1330	1335	1340
Val Asn Lys Ala Asn Arg Phe Thr Val Glu Thr Arg Gly Ala Gly Thr			
1345	1350	1355	1360
Gly Gly Leu Gly Leu Ala Ile Glu Gly Pro Ser Glu Ala Lys Met Ser			
	1365	1370	1375
Cys Lys Asp Asn Lys Asp Gly Ser Cys Thr Val Glu Tyr Ile Pro Phe			
	1380	1385	1390

Thr Pro Gly Asp Tyr Asp Val Asn Ile Thr Phe Gly Gly Arg Pro Ile
1395 1400 1405

Pro Gly Ser Pro Phe Arg Val Pro Val Lys Asp Val Val Asp Pro Gly
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Lys Val Lys Cys Ser Gly Pro Gly Leu Gly Ala Gly Val Arg Ala Arg
1425 1430 1435 1440

Val Pro Gln Thr Phe Thr Val Asp Cys Ser Gln Ala Gly Arg Ala Pro
1445 1450 1455

Leu Gln Val Ala Val Leu Gly Pro Thr Gly Val Ala Glu Pro Val Glu
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Val Arg Asp Asn Gly Asp Gly Thr His Thr Val His Tyr Thr Pro Ala
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Thr Asp Gly Pro Tyr Thr Val Ala Val Lys Tyr Ala Asp Gln Glu Val
1490 1495 1500

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Lys Val Arg Ala Ser Gly Pro Gly Leu Asn Ala Ser Gly Ile Pro Ala
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Ser Leu Pro Val Glu Phe Thr Ile Asp Ala Arg Asp Ala Gly Glu Gly
1540 1545 1550

Leu Leu Thr Val Gln Ile Leu Gly Pro Glu Gly Lys Pro Lys Lys Ala
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Asn Ile Arg Asp Asn Gly Asp Gly Thr Tyr Ala Val Ser Tyr Leu Pro
1570 1575 1580

Asp Met Ser Gly Arg Tyr Thr Ile Thr Ile Lys Tyr Gly Gly Asp Glu
1585 1590 1595 1600

Ile Pro Tyr Ser Pro Phe Arg Ile His Ala Leu Pro Thr Gly Asp Ala
1605 1610 1615

Ser Lys Cys Leu Val Thr Val Ser Ile Gly Gly His Gly Leu Gly Ala
1620 1625 1630

Cys Leu Gly Pro Arg Ile Gln Ile Gly Gln Glu Thr Val Ile Thr Val
1635 1640 1645

Asp Ala Lys Ala Ala Gly Glu Gly Lys Val Thr Cys Thr Val Ser Thr
1650 1655 1660

Pro Asp Gly Ala Glu Leu Asp Val Asp Val Val Glu Asn His Asp Gly
1665 1670 1675 1680

Thr Phe Asp Ile Tyr Tyr Thr Ala Pro Glu Pro Gly Lys Tyr Val Ile
1685 1690 1695

Thr Ile Arg Phe Gly Gly Glu His Ile Pro Asn Ser Pro Phe His Val
1700 1705 1710

Leu Ala Cys Asp Pro Leu Pro His Glu Glu Glu Pro Ser Glu Val Pro
1715 1720 1725

Gln Leu Arg Gln Pro Tyr Ala Pro Pro Arg Pro Gly Ala Arg Pro Thr
1730 1735 1740

His Trp Ala Thr Glu Glu Pro Val Val Pro Val Glu Pro Met Glu Ser
1745 1750 1755 1760

Met Leu Arg Pro Phe Asn Leu Val Ile Pro Phe Ala Val Gln Lys Gly
1765 1770 1775

Glu Leu Thr Gly Glu Val Arg Met Pro Ser Gly Lys Thr Ala Arg Pro
1780 1785 1790

Asn Ile Thr Asp Asn Lys Asp Gly Thr Ile Thr Val Arg Tyr Ala Pro
1795 1800 1805

Thr Glu Lys Gly Leu His Gln Met Gly Ile Lys Tyr Asp Gly Asn His

1810	1815	1820	
Ile Pro Gly Ser Pro Leu Gln Phe Tyr Val Asp Ala Ile Asn Ser Arg			
1825	1830	1835	1840
His Val Ser Ala Tyr Gly Pro Gly Leu Ser His Gly Met Val Asn Lys			
1845	1850	1855	
Pro Ala Thr Phe Thr Ile Val Thr Lys Asp Ala Gly Glu Gly Gly Leu			
1860	1865	1870	
Ser Leu Ala Val Glu Gly Pro Ser Lys Ala Glu Ile Thr Cys Lys Asp			
1875	1880	1885	
Asn Lys Asp Gly Thr Cys Thr Val Ser Tyr Leu Pro Thr Ala Pro Gly			
1890	1895	1900	
Asp Tyr Ser Ile Ile Val Arg Phe Asp Asp Lys His Ile Pro Gly Ser			
1905	1910	1915	1920
Pro Phe Thr Ala Lys Ile Thr Gly Asp Asp Ser Met Arg Thr Ser Gln			
1925	1930	1935	
Leu Asn Val Gly Thr Ser Thr Asp Val Ser Leu Lys Ile Thr Glu Ser			
1940	1945	1950	
Asp Leu Ser Gln Leu Thr Ala Ser Ile Arg Ala Pro Ser Gly Asn Glu			
1955	1960	1965	
Glu Pro Cys Leu Leu Lys Arg Leu Pro Asn Arg His Ile Gly Ile Ser			
1970	1975	1980	
Phe Thr Pro Lys Glu Val Gly Glu His Val Val Ser Val Arg Lys Ser			
1985	1990	1995	2000
Gly Lys His Val Thr Asn Ser Pro Phe Lys Ile Leu Val Gly Pro Ser			
2005	2010	2015	
Glu Ile Gly Asp Ala Ser Lys Val Arg Val Trp Gly Lys Gly Leu Ser			

2020	2025	2030	
Glu Gly His Thr Phe Gln Val Ala Glu Phe Ile Val Asp Thr Arg Asn			
2035	2040	2045	
Ala Gly Tyr Gly Gly Leu Gly Leu Ser Ile Glu Gly Pro Ser Lys Val			
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Asp Ile Asn Cys Glu Asp Met Glu Asp Gly Thr Cys Lys Val Thr Tyr			
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Cys Pro Thr Glu Pro Gly Thr Tyr Ile Ile Asn Ile Lys Phe Ala Asp			
2085	2090	2095	
Lys His Val Pro Gly Ser Pro Phe Thr Val Lys Val Thr Gly Glu Gly			
2100	2105	2110	
Arg Met Lys Glu Ser Ile Thr Arg Arg Arg Gln Ala Pro Ser Ile Ala			
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Thr Ile Gly Ser Thr Cys Asp Leu Asn Leu Lys Ile Pro Gly Asn Trp			
2130	2135	2140	
Phe Gln Met Val Ser Ala Gln Glu Arg Leu Thr Arg Thr Phe Thr Arg			
2145	2150	2155	2160
Ser Ser His Thr Tyr Thr Arg Thr Glu Arg Thr Glu Ile Ser Lys Thr			
2165	2170	2175	
Arg Gly Gly Glu Thr Lys Pro Glu Val Arg Val Glu Glu Ser Thr Gln			
2180	2185	2190	
Val Gly Gly Asp Pro Phe Pro Ala Val Phe Gly Asp Phe Leu Gly Arg			
2195	2200	2205	
Glu Arg Leu Gly Ser Phe Gly Ser Ile Thr Arg Gln Gln Glu Gly Glu			
2210	2215	2220	
Ala Ser Ser Gln Asp Met Thr Ala Gln Val Thr Ser Pro Ser Gly Lys			
2225	2230	2235	2240

Val Glu Ala Ala Glu Ile Val Glu Gly Glu Asp Ser Ala Tyr Ser Val

2245

2250

2255

Arg Phe Val Pro Gln Glu Met Gly Pro His Thr Val Ala Val Lys Tyr

2260

2265

2270

Arg Gly Gln His Val Pro Gly Ser Pro Phe Gln Phe Thr Val Gly Pro

2275

2280

2285

Leu Gly Glu Gly Gly Ala His Lys Val Arg Ala Gly Arg Ala Gly Leu

2290

2295

2300

Glu Arg Gly Val Ala Gly Val Pro Ala Glu Phe Ser Ile Trp Thr Arg

2305

2310

2315

2320

Glu Ala Gly Ala Gly Gly Leu Ser Ile Ala Val Glu Gly Pro Ser Lys

2325

2330

2335

Ala Glu Ile Ala Phe Glu Asp Arg Lys Asp Gly Ser Cys Gly Val Ser

2340

2345

2350

Tyr Val Val Gln Glu Pro Gly Asp Tyr Glu Val Ser Ile Lys Phe Asn

2355

2360

2365

Asp Glu His Ile Pro Asp Ser Pro Phe Val Val Pro Val Ala Ser Leu

2370

2375

2380

Ser Asp Asp Ala Arg Arg Leu Thr Val Thr Ser Leu Gln Glu Thr Gly

2385

2390

2395

2400

Leu Lys Val Asn Gln Pro Ala Ser Phe Ala Val Gln Leu Asn Gly Ala

2405

2410

2415

Arg Gly Val Ile Asp Ala Arg Val His Thr Pro Ser Gly Ala Val Glu

2420

2425

2430

Glu Cys Tyr Val Ser Glu Leu Asp Ser Asp Lys His Thr Ile Arg Phe

2435

2440

2445

Ile Pro His Glu Asn Gly Val His Ser Ile Asp Val Lys Phe Asn Gly
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 Ala His Ile Pro Gly Ser Pro Phe Lys Ile Arg Val Gly Glu Gln Ser
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 Gln Ala Gly Asp Pro Gly Leu Val Ser Ala Tyr Gly Pro Gly Leu Glu
 2485 2490 2495
 Gly Gly Thr Thr Gly Val Ser Ser Glu Phe Ile Val Asn Thr Leu Asn
 2500 2505 2510
 Ala Gly Ser Gly Ala Leu Ser Val Thr Ile Asp Gly Pro Ser Lys Val
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 Gln Leu Asp Cys Arg Glu Cys Pro Glu Gly His Val Val Thr Tyr Thr
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 Pro Met Ala Pro Gly Asn Tyr Leu Ile Ala Ile Lys Tyr Gly Gly Pro
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 Gln His Ile Val Gly Ser Pro Phe Lys Ala Lys Val Thr Gly Pro Arg
 2565 2570 2575
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 2580 2585 2590
 Thr Val Thr Lys Ser Ser Ser Ser Arg Gly Ser Ser Tyr Ser Ser Ile
 2595 2600 2605
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 2610 2615 2620
 Leu Ser Gln Ala Phe Val Gly Gln Lys Asn Ser Phe Thr Val Asp Cys
 2625 2630 2635 2640
 Ser Lys Ala Gly Thr Asn Met Met Met Val Gly Val His Gly Pro Lys
 2645 2650 2655
 Thr Pro Cys Glu Glu Val Tyr Val Lys His Met Gly Asn Arg Val Tyr

2660 2665 2670
 Asn Val Thr Tyr Thr Val Lys Glu Lys Gly Asp Tyr Ile Leu Ile Val

2675 2680 2685
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 Pro

2705

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<211> 2016

<212> DNA

<213> Homo sapiens

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<221> CDS

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 gaccccgctg cgcacggcct gtccgctgca caccagcttg ttggcgctct cgtcgccgcg 180
 ctgccccggg gctactcctg cgcgccaca atg agc tcc cgc atc gcc agg gcg 233

Met Ser Ser Arg Ile Ala Arg Ala

1

5

ctc gcc tta gtc gtc acc ctt ctc cac ttg acc agg ctg gcg ctc tcc 281
 Leu Ala Leu Val Val Thr Leu Leu His Leu Thr Arg Leu Ala Leu Ser

10

15

20

acc tgc ccc gct gcc tgc cac tgc ccc ctg gag gcg ccc aag tgc gcg 329
 Thr Cys Pro Ala Ala Cys His Cys Pro Leu Glu Ala Pro Lys Cys Ala

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Pro Gly Val Gly Leu Val Arg Asp Gly Cys Gly Cys Cys Lys Val Cys				
45	50	55		
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Ala Lys Gln Leu Asn Glu Asp Cys Ser Lys Thr Gln Pro Cys Asp His				
60	65	70		
acc aag ggg ctg gaa tgc aac ttc ggc gcc agc tcc acc gct ctg aag	473			
Thr Lys Gly Leu Glu Cys Asn Phe Gly Ala Ser Ser Thr Ala Leu Lys				
75	80	85		
ggg atc tgc aga gct cag tca gag ggc aga ccc tgt gaa tat aac tcc	521			
Gly Ile Cys Arg Ala Gln Ser Glu Gly Arg Pro Cys Glu Tyr Asn Ser				
90	95	100		
aga atc tac caa aac ggg gaa agt ttc cag ccc aac tgt aaa cat cag	569			
Arg Ile Tyr Gln Asn Gly Glu Ser Phe Gln Pro Asn Cys Lys His Gln				
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tgc aca tgt att gat ggc gcc gtg ggc tgc att cct ctg tgt ccc caa	617			
Cys Thr Cys Ile Asp Gly Ala Val Gly Cys Ile Pro Leu Cys Pro Gln				
125	130	135		
gaa cta tct ctc ccc aac ttg ggc tgt ccc aac cct cgg ctg gtc aaa	665			
Glu Leu Ser Leu Pro Asn Leu Gly Cys Pro Asn Pro Arg Leu Val Lys				
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gtt acc ggg cag tgc tgc gag gag tgg gtc tgt gac gag gat agt atc	713			
Val Thr Gly Gln Cys Cys Glu Glu Trp Val Cys Asp Glu Asp Ser Ile				
155	160	165		
aag gac ccc atg gag gac cag gac ggc ctc ctt ggc aag gag ctg gga	761			

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 Phe Asp Ala Ser Glu Val Glu Leu Thr Arg Asn Asn Glu Leu Ile Ala
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 Val Gly Lys Gly Ser Ser Leu Lys Arg Leu Pro Val Phe Gly Met Glu
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 Pro Arg Ile Leu Tyr Asn Pro Leu Gln Gly Gln Lys Cys Ile Val Gln
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 aca act tca tgg tcc cag tgc tca aag acc tgt gga act ggt atc tcc 953
 Thr Thr Ser Trp Ser Gln Cys Ser Lys Thr Cys Gly Thr Gly Ile Ser
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 Thr Arg Val Thr Asn Asp Asn Pro Glu Cys Arg Leu Val Lys Glu Thr
 250 255 260
 cgg att tgt gag gtg cgg cct tgt gga cag cca gtg tac agc agc ctg 1049
 Arg Ile Cys Glu Val Arg Pro Cys Gly Gln Pro Val Tyr Ser Ser Leu
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 Arg Phe Thr Tyr Ala Gly Cys Leu Ser Val Lys Lys Tyr Arg Pro Lys
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Tyr Cys Gly Ser Cys Val Asp Gly Arg Cys Cys Thr Pro Gln Leu Thr
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 Lys Asn Val Met Met Ile Gln Ser Cys Lys Cys Asn Tyr Asn Cys Pro
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 His Ala Asn Glu Ala Ala Phe Pro Phe Tyr Arg Leu Phe Asn Asp Ile
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 His Lys Phe Arg Asp
 380
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<212> PRT

<213> Homo sapiens

<400> 46

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35 40 45
Gly Cys Gly Cys Cys Lys Val Cys Ala Lys Gln Leu Asn Glu Asp Cys
50 55 60
Ser Lys Thr Gln Pro Cys Asp His Thr Lys Gly Leu Glu Cys Asn Phe
65 70 75 80
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85 90 95
Gly Arg Pro Cys Glu Tyr Asn Ser Arg Ile Tyr Gln Asn Gly Glu Ser
100 105 110
Phe Gln Pro Asn Cys Lys His Gln Cys Thr Cys Ile Asp Gly Ala Val
115 120 125
Gly Cys Ile Pro Leu Cys Pro Gln Glu Leu Ser Leu Pro Asn Leu Gly
130 135 140
Cys Pro Asn Pro Arg Leu Val Lys Val Thr Gly Gln Cys Cys Glu Glu
145 150 155 160
Trp Val Cys Asp Glu Asp Ser Ile Lys Asp Pro Met Glu Asp Gln Asp
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Gly Leu Leu Gly Lys Glu Leu Gly Phe Asp Ala Ser Glu Val Glu Leu
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 Thr Arg Asn Asn Glu Leu Ile Ala Val Gly Lys Gly Ser Ser Leu Lys
 195 200 205
 Arg Leu Pro Val Phe Gly Met Glu Pro Arg Ile Leu Tyr Asn Pro Leu
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 Gln Gly Gln Lys Cys Ile Val Gln Thr Thr Ser Trp Ser Gln Cys Ser
 225 230 235 240
 Lys Thr Cys Gly Thr Gly Ile Ser Thr Arg Val Thr Asn Asp Asn Pro
 245 250 255
 Glu Cys Arg Leu Val Lys Glu Thr Arg Ile Cys Glu Val Arg Pro Cys
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 Gly Gln Pro Val Tyr Ser Ser Leu Lys Lys Gly Lys Lys Cys Ser Lys
 275 280 285
 Thr Lys Lys Ser Pro Glu Pro Val Arg Phe Thr Tyr Ala Gly Cys Leu
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 Ser Val Lys Lys Tyr Arg Pro Lys Tyr Cys Gly Ser Cys Val Asp Gly
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<213> Homo sapiens

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atg cca agc acc agc ttt cca gtc cct tcc aag ttt cca ctt ggc cct 287
Met Pro Ser Thr Ser Phe Pro Val Pro Ser Lys Phe Pro Leu Gly Pro
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Ala Gly Gly Thr Met Lys Ser Ala Glu Glu Glu His Tyr Gly Tyr Ala
      35          40          45
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Ser Ser Asn Val Ser Pro Ala Leu Pro Leu Pro Thr Ala His Ser Thr
      50          55          60
ctg ccg gcc ccg tgc cac aac ctt cag acc tcc aca ccg ggc atc atc 479
Leu Pro Ala Pro Cys His Asn Leu Gln Thr Ser Thr Pro Gly Ile Ile
      65          70          75          80

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 Pro Ala Gly Tyr Phe Leu Ser Ser Gly His Thr Arg Pro Asp Gly Ala
 100 105 110
 cct gcc ctg gag agt cct cgc atc gag ata acc tcg tgc ttg ggc ctg 623
 Pro Ala Leu Glu Ser Pro Arg Ile Glu Ile Thr Ser Cys Leu Gly Leu
 115 120 125
 tac cac aac aat aac cag ttt ttc cac gat gtg gag gtg gaa gac gtc 671
 Tyr His Asn Asn Asn Gln Phe Phe His Asp Val Glu Val Glu Asp Val
 130 135 140
 ctc cct agc tcc aaa cgg tcc ccc tcc acg gcc acg ctg agt ctg ccc 719
 Leu Pro Ser Ser Lys Arg Ser Pro Ser Thr Ala Thr Leu Ser Leu Pro
 145 150 155 160
 agc ctg gag gcc tac aga gac ccc tcg tgc ctg agc ccg gcc agc agc 767
 Ser Leu Glu Ala Tyr Arg Asp Pro Ser Cys Leu Ser Pro Ala Ser Ser
 165 170 175
 ctg tcc tcc cgg agc tgc aac tca gag gcc tcc tcc tac gag tcc aac 815
 Leu Ser Ser Arg Ser Cys Asn Ser Glu Ala Ser Ser Tyr Glu Ser Asn
 180 185 190
 tac tcg tac ccg tac gcg tcc ccc cag acg tcg cca tgg cag tct ccc 863
 Tyr Ser Tyr Pro Tyr Ala Ser Pro Gln Thr Ser Pro Trp Gln Ser Pro
 195 200 205
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 Cys Val Ser Pro Lys Thr Thr Asp Pro Glu Glu Gly Phe Pro Arg Gly

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Leu Gly Ala Cys Thr Leu Leu Gly Ser Pro Gln His Ser Pro Ser Thr			
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tcc ccc cgc gcc agc gtc act gag gag agc tgg ctg ggt gcc cgc tcc	1007		
Ser Pro Arg Ala Ser Val Thr Glu Glu Ser Trp Leu Gly Ala Arg Ser			
245	250	255	
tcc aga ccc gcg tcc cct tgc aac aag agg aag tac agc ctc aac ggc	1055		
Ser Arg Pro Ala Ser Pro Cys Asn Lys Arg Lys Tyr Ser Leu Asn Gly			
260	265	270	
cgg cag ccg ccc tac tca ccc cac cac tcc ccc acg ccg tcc ccg cac	1103		
Arg Gln Pro Pro Tyr Ser Pro His His Ser Pro Thr Pro Ser Pro His			
275	280	285	
ggc tcc ccg cgg gtc agc gtg acc gac gac tcc tgg ttg ggc aac acc	1151		
Gly Ser Pro Arg Val Ser Val Thr Asp Asp Ser Trp Leu Gly Asn Thr			
290	295	300	
acc cag tac acc agc tcc gcc atc gtg gcc gcc atc aac gcg ctg acc	1199		
Thr Gln Tyr Thr Ser Ser Ala Ile Val Ala Ala Ile Asn Ala Leu Thr			
305	310	315	320
acc gac agc agc ctg gac ctg gga gat ggc gtc cct gtc aag tcc cgc	1247		
Thr Asp Ser Ser Leu Asp Leu Gly Asp Gly Val Pro Val Lys Ser Arg			
325	330	335	
aag acc acc ctg gag cag ccg ccc tca gtg gcg ctc aag gtg gag ccc	1295		
Lys Thr Thr Leu Glu Gln Pro Pro Ser Val Ala Leu Lys Val Glu Pro			
340	345	350	
gtc ggg gag gac ctg ggc agc ccc ccg ccc ccg gcc gac ttc gcg ccc	1343		
Val Gly Glu Asp Leu Gly Ser Pro Pro Pro Pro Ala Asp Phe Ala Pro			

355	360	365	
gaa gac tac tcc tct ttc cag cac atc agg aag ggc ggc ttc tgc gac			1391
Glu Asp Tyr Ser Ser Phe Gln His Ile Arg Lys Gly Gly Phe Cys Asp			
370	375	380	
cag tac ctg gcg gig ccg cag cac ccc tac cag tgg gcg aag ccc aag			1439
Gln Tyr Leu Ala Val Pro Gln His Pro Tyr Gln Trp Ala Lys Pro Lys			
385	390	395	400
ccc ctg tcc cct acg tcc tac atg agc ccg acc ctg ccc gcc ctg gac			1487
Pro Leu Ser Pro Thr Ser Tyr Met Ser Pro Thr Leu Pro Ala Leu Asp			
405	410	415	
tgg cag ctg ccg tcc cac tca ggc ccg tat gag ctt cgg att gag gtg			1535
Trp Gln Leu Pro Ser His Ser Gly Pro Tyr Glu Leu Arg Ile Glu Val			
420	425	430	
cag ccc aag tcc cac cac cga gcc cac tac gag acg gag ggc agc ccg			1583
Gln Pro Lys Ser His His Arg Ala His Tyr Glu Thr Glu Gly Ser Arg			
435	440	445	
ggg gcc gtg aag gcg tcg gcc gga gga cac ccc atc gtg cag ctg cat			1631
Gly Ala Val Lys Ala Ser Ala Gly Gly His Pro Ile Val Gln Leu His			
450	455	460	
ggc tac ttg gag aat gag ccg ctg atg ctg cag ctt ttc att ggg acg			1679
Gly Tyr Leu Glu Asn Glu Pro Leu Met Leu Gln Leu Phe Ile Gly Thr			
465	470	475	480
gcg gac gac cgc ctg ctg cgc ccg cac gcc ttc tac cag gtg cac cgc			1727
Ala Asp Asp Arg Leu Leu Arg Pro His Ala Phe Tyr Gln Val His Arg			
485	490	495	
atc aca ggg aag acc gtg tcc acc acc agc cac gag gct atc ctc tcc			1775

Ile Thr Gly Lys Thr Val Ser Thr Thr Ser His Glu Ala Ile Leu Ser
 500 505 510
 aac acc aaa gtc ctg gag atc cca ctc ctg ccg gag aac agc atg cga 1823
 Asn Thr Lys Val Leu Glu Ile Pro Leu Leu Pro Glu Asn Ser Met Arg
 515 520 525
 gcc gtc att gac tgt gcc gga atc ctg aaa ctc aga aac tcc gac att 1871
 Ala Val Ile Asp Cys Ala Gly Ile Leu Lys Leu Arg Asn Ser Asp Ile
 530 535 540
 gaa ctt cgg aaa gga gag acg gac atc ggg agg aag aac aca cgg gta 1919
 Glu Leu Arg Lys Gly Glu Thr Asp Ile Gly Arg Lys Asn Thr Arg Val
 545 550 555 560
 cgg ctg gtg ttc cgc gtt cac gtc ccg caa ccc agc ggc cgc acg ctg 1967
 Arg Leu Val Phe Arg Val His Val Pro Gln Pro Ser Gly Arg Thr Leu
 565 570 575
 tcc ctg cag gtg gcc tcc aac ccc atc gaa tgc tcc cag cgc tca gct 2015
 Ser Leu Gln Val Ala Ser Asn Pro Ile Glu Cys Ser Gln Arg Ser Ala
 580 585 590
 cag gag ctg cct ctg gtg gag aag cag agc acg gac agc tat ccg gtc 2063
 Gln Glu Leu Pro Leu Val Glu Lys Gln Ser Thr Asp Ser Tyr Pro Val
 595 600 605
 gtg ggc ggg aag aag atg gtc ctg tct ggc cac aac ttc ctg cag gac 2111
 Val Gly Gly Lys Lys Met Val Leu Ser Gly His Asn Phe Leu Gln Asp
 610 615 620
 tcc aag gtc att ttc gtg gag aaa gcc cca gat ggc cac cat gtc tgg 2159
 Ser Lys Val Ile Phe Val Glu Lys Ala Pro Asp Gly His His Val Trp
 625 630 635 640
 gag atg gaa gcg aaa act gac cgg gac ctg tgc aag ccg aat tct ctg 2207

Glu Met Glu Ala Lys Thr Asp Arg Asp Leu Cys Lys Pro Asn Ser Leu
 645 650 655
 gtg gtt gag atc ccg cca ttt cgg aat cag agg ata acc agc ccc gtt 2255
 Val Val Glu Ile Pro Pro Phe Arg Asn Gln Arg Ile Thr Ser Pro Val
 660 665 670
 cac gtc agt ttc tac glc tgc aac ggg aag aga aag cga agc cag tac 2303
 His Val Ser Phe Tyr Val Cys Asn Gly Lys Arg Lys Arg Ser Gln Tyr
 675 680 685
 cag cgt ttc acc tac ctt ccc gcc aac ggt aac gcc atc ttt cta acc 2351
 Gln Arg Phe Thr Tyr Leu Pro Ala Asn Gly Asn Ala Ile Phe Leu Thr
 690 695 700
 gta agc cgt gaa cat gag cgc gtg ggg tgc ttt ttc taaagacgca 2397
 Val Ser Arg Glu His Glu Arg Val Gly Cys Phe Phe
 705 710 715
 gaaacgacgt cgccgtaaag cagcgtggcg tgttgcacat ttaactgtgt gatgtcccg 2457
 tagtagagacc gagccatcga tgcctgaaa aggaaaggaa aagggaagct tcggatgcat 2517
 tttccttgat cctgttggg ggtagggggc gggggttgca tactcagata gtcacggta 2577
 ttttgcttct tgcgaatgta taacagccaa ggggaaaaca tggctcttct gctccaaaaa 2637
 actgaggggg tcctggtgtg catttgcacc ctaaagctgc ttacggtgaa aaggcaaata 2697
 ggtatagcta ttttgcaggc accttagga ataaactttg ctttta 2743

<210> 48

<211> 716

<212> PRT

<213> Homo sapiens

<400> 48

Met Pro Ser Thr Ser Phe Pro Val Pro Ser Lys Phe Pro Leu Gly Pro

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20 25 30
Ala Gly Gly Thr Met Lys Ser Ala Glu Glu Glu His Tyr Gly Tyr Ala
35 40 45
Ser Ser Asn Val Ser Pro Ala Leu Pro Leu Pro Thr Ala His Ser Thr
50 55 60
Leu Pro Ala Pro Cys His Asn Leu Gln Thr Ser Thr Pro Gly Ile Ile
65 70 75 80
Pro Pro Ala Asp His Pro Ser Gly Tyr Gly Ala Ala Leu Asp Gly Gly
85 90 95
Pro Ala Gly Tyr Phe Leu Ser Ser Gly His Thr Arg Pro Asp Gly Ala
100 105 110
Pro Ala Leu Glu Ser Pro Arg Ile Glu Ile Thr Ser Cys Leu Gly Leu
115 120 125
Tyr His Asn Asn Asn Gln Phe Phe His Asp Val Glu Val Glu Asp Val
130 135 140
Leu Pro Ser Ser Lys Arg Ser Pro Ser Thr Ala Thr Leu Ser Leu Pro
145 150 155 160
Ser Leu Glu Ala Tyr Arg Asp Pro Ser Cys Leu Ser Pro Ala Ser Ser
165 170 175
Leu Ser Ser Arg Ser Cys Asn Ser Glu Ala Ser Ser Tyr Glu Ser Asn
180 185 190
Tyr Ser Tyr Pro Tyr Ala Ser Pro Gln Thr Ser Pro Trp Gln Ser Pro
195 200 205
Cys Val Ser Pro Lys Thr Thr Asp Pro Glu Glu Gly Phe Pro Arg Gly

210 215 220
Leu Gly Ala Cys Thr Leu Leu Gly Ser Pro Gln His Ser Pro Ser Thr
225 230 235 240
Ser Pro Arg Ala Ser Val Thr Glu Glu Ser Trp Leu Gly Ala Arg Ser
245 250 255
Ser Arg Pro Ala Ser Pro Cys Asn Lys Arg Lys Tyr Ser Leu Asn Gly
260 265 270
Arg Gln Pro Pro Tyr Ser Pro His His Ser Pro Thr Pro Ser Pro His
275 280 285
Gly Ser Pro Arg Val Ser Val Thr Asp Asp Ser Trp Leu Gly Asn Thr
290 295 300
Thr Gln Tyr Thr Ser Ser Ala Ile Val Ala Ala Ile Asn Ala Leu Thr
305 310 315 320
Thr Asp Ser Ser Leu Asp Leu Gly Asp Gly Val Pro Val Lys Ser Arg
325 330 335
Lys Thr Thr Leu Glu Gln Pro Pro Ser Val Ala Leu Lys Val Glu Pro
340 345 350
Val Gly Glu Asp Leu Gly Ser Pro Pro Pro Pro Ala Asp Phe Ala Pro
355 360 365
Glu Asp Tyr Ser Ser Phe Gln His Ile Arg Lys Gly Gly Phe Cys Asp
370 375 380
Gln Tyr Leu Ala Val Pro Gln His Pro Tyr Gln Trp Ala Lys Pro Lys
385 390 395 400
Pro Leu Ser Pro Thr Ser Tyr Met Ser Pro Thr Leu Pro Ala Leu Asp
405 410 415
Trp Gln Leu Pro Ser His Ser Gly Pro Tyr Glu Leu Arg Ile Glu Val
420 425 430

Gln Pro Lys Ser His His Arg Ala His Tyr Glu Thr Glu Gly Ser Arg
 435 440 445
 Gly Ala Val Lys Ala Ser Ala Gly Gly His Pro Ile Val Gln Leu His
 450 455 460
 Gly Tyr Leu Glu Asn Glu Pro Leu Met Leu Gln Leu Phe Ile Gly Thr
 465 470 475 480
 Ala Asp Asp Arg Leu Leu Arg Pro His Ala Phe Tyr Gln Val His Arg
 485 490 495
 Ile Thr Gly Lys Thr Val Ser Thr Thr Ser His Glu Ala Ile Leu Ser
 500 505 510
 Asn Thr Lys Val Leu Glu Ile Pro Leu Leu Pro Glu Asn Ser Met Arg
 515 520 525
 Ala Val Ile Asp Cys Ala Gly Ile Leu Lys Leu Arg Asn Ser Asp Ile
 530 535 540
 Glu Leu Arg Lys Gly Glu Thr Asp Ile Gly Arg Lys Asn Thr Arg Val
 545 550 555 560
 Arg Leu Val Phe Arg Val His Val Pro Gln Pro Ser Gly Arg Thr Leu
 565 570 575
 Ser Leu Gln Val Ala Ser Asn Pro Ile Glu Cys Ser Gln Arg Ser Ala
 580 585 590
 Gln Glu Leu Pro Leu Val Glu Lys Gln Ser Thr Asp Ser Tyr Pro Val
 595 600 605
 Val Gly Gly Lys Lys Met Val Leu Ser Gly His Asn Phe Leu Gln Asp
 610 615 620
 Ser Lys Val Ile Phe Val Glu Lys Ala Pro Asp Gly His His Val Trp
 625 630 635 640

Glu Met Glu Ala Lys Thr Asp Arg Asp Leu Cys Lys Pro Asn Ser Leu

645

650

655

Val Val Glu Ile Pro Pro Phe Arg Asn Gln Arg Ile Thr Ser Pro Val

660

665

670

His Val Ser Phe Tyr Val Cys Asn Gly Lys Arg Lys Arg Ser Gln Tyr

675

680

685

Gln Arg Phe Thr Tyr Leu Pro Ala Asn Gly Asn Ala Ile Phe Leu Thr

690

695

700

Val Ser Arg Glu His Glu Arg Val Gly Cys Phe Phe

705

710

715

<210> 49

<211> 2353

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (241).. (1482)

<400> 49

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gggaagcccc gccgccgccg ccccgccgc cccctcccc gccgccgcc cccctcccc 120

ccgcccgtc gccgccctc tccctctgcc tccctcccc acggccggcc gccctctgc 180

ccgccgccgc gcagccgagg agccgaggcc gccgccggcc tggcggcgga gccctcagcc 240

atg gcc tcg ggc gac acc ctc tac atc gcc acg gac ggc tcg gag atg 288

Met Ala Ser Gly Asp Thr Leu Tyr Ile Ala Thr Asp Gly Ser Glu Met

1

5

10

15

ccg gcc gag atc gtg gag ctg cac gag atc gag gtg gag acc atc ccg 336

Pro Ala Glu Ile Val Glu Leu His Glu Ile Glu Val Glu Thr Ile Pro
 20 25 30
 gtg gag acc atc gag acc aca gtg gtg ggc gag gag gag gag gag gag gac 384
 Val Glu Thr Ile Glu Thr Thr Val Val Gly Glu Glu Glu Glu Glu Asp
 35 40 45
 gac gag gag gag gag ggc ggc ggt ggc gag cac ggc ggc ggc ggc ggc 432
 Asp Asp Asp Glu Asp Gly Gly Gly Gly Asp His Gly Gly Gly Gly Gly
 50 55 60
 cac ggc cac gcc ggc cac cac cac cac cac cat cac cac cac cac cac 480
 His Gly His Ala Gly His His His His His His His His His His His
 65 70 75 80
 ccg ccc atg atc gct ctg cag ccg ctg gtc acc gag gag ccg acc cag 528
 Pro Pro Met Ile Ala Leu Gln Pro Leu Val Thr Asp Asp Pro Thr Gln
 85 90 95
 gtg cac cac cac cag gag gtg atc ctg gtg cag acg cgc gag gag gtg 576
 Val His His His Gln Glu Val Ile Leu Val Gln Thr Arg Glu Glu Val
 100 105 110
 gtg ggc ggc gag gag tcg gag ggc ctg cgc gcc gag gag ggc ttc gag 624
 Val Gly Gly Asp Asp Ser Asp Gly Leu Arg Ala Glu Asp Gly Phe Glu
 115 120 125
 gat cag att ctc atc ccg gtg ccc gcg ccg gcc ggc ggc gag gag gag 672
 Asp Gln Ile Leu Ile Pro Val Pro Ala Pro Ala Gly Gly Asp Asp Asp
 130 135 140
 tac att gaa caa acg ctg gtc acc gtg gcg gcg gcc ggc aag agc ggc 720
 Tyr Ile Glu Gln Thr Leu Val Thr Val Ala Ala Ala Gly Lys Ser Gly
 145 150 155 160
 ggc ggc ggc tcg tcg tcg tcg gga ggc ggc cgc gtc aag aag ggc ggc 768

Gly Gly Gly Ser Ser Ser Ser Gly Gly Gly Arg Val Lys Lys Gly Gly
 165 170 175
 ggc aag aag agc ggc aag aag agt tac ctc agc ggc ggc gcc ggc gcg 816
 Gly Lys Lys Ser Gly Lys Lys Ser Tyr Leu Ser Gly Gly Ala Gly Ala
 180 185 190
 gcg ggc ggc cgc ggc gcc gac ccg ggc aac aag aag tgg gag cag aag 864
 Ala Gly Gly Arg Gly Ala Asp Pro Gly Asn Lys Lys Trp Glu Gln Lys
 195 200 205
 cag gtg cag atc aag acc ctg gag ggc gag ttc tcg gtc acc atg tgg 912
 Gln Val Gln Ile Lys Thr Leu Glu Gly Glu Phe Ser Val Thr Met Trp
 210 215 220
 tcc tca gat gaa aaa aaa gat att gac cat gag aca gtg gtt gaa gaa 960
 Ser Ser Asp Glu Lys Lys Asp Ile Asp His Glu Thr Val Val Glu Glu
 225 230 235 240
 cag atc att gga gag aac tca cct cct gat tat tca gaa tat atg aca 1008
 Gln Ile Ile Gly Glu Asn Ser Pro Pro Asp Tyr Ser Glu Tyr Met Thr
 245 250 255
 gga aag aaa ctt cct cct gga gga ala cct ggc att gac ctc tca gat 1056
 Gly Lys Lys Leu Pro Pro Gly Gly Ile Pro Gly Ile Asp Leu Ser Asp
 260 265 270
 ccc aaa caa ctg gca gaa ttt gct aga atg aag cca aga aaa att aaa 1104
 Pro Lys Gln Leu Ala Glu Phe Ala Arg Met Lys Pro Arg Lys Ile Lys
 275 280 285
 gaa gat gat gct cca aga aca ata gct tgc cct cat aaa ggc tgc aca 1152
 Glu Asp Asp Ala Pro Arg Thr Ile Ala Cys Pro His Lys Gly Cys Thr
 290 295 300

aag atg ttc agg gat aac tcg gcc atg aga aaa cat ctg cac acc cac 1200
Lys Met Phe Arg Asp Asn Ser Ala Met Arg Lys His Leu His Thr His
305 310 315 320
ggc ccc aga gtc cac gtc tgt gca gaa tgt ggc aaa gct ttt gtt gag 1248
Gly Pro Arg Val His Val Cys Ala Glu Cys Gly Lys Ala Phe Val Glu
325 330 335
agt tca aaa cta aaa cga cac caa ctg gtt cat act gga gag aag ccc 1296
Ser Ser Lys Leu Lys Arg His Gln Leu Val His Thr Gly Glu Lys Pro
340 345 350
ttt cag tgc acg ttc gaa ggc tgt ggg aaa cgc ttt tca ctg gac ttc 1344
Phe Gln Cys Thr Phe Glu Gly Cys Gly Lys Arg Phe Ser Leu Asp Phe
355 360 365
aat ttg cgc aca cat gtg cga atc cat acc gga gac agg ccc tat gtg 1392
Asn Leu Arg Thr His Val Arg Ile His Thr Gly Asp Arg Pro Tyr Val
370 375 380
tgc ccc ttc gat ggt tgt aat aag aag ttt gct cag tca act aac ctg 1440
Cys Pro Phe Asp Gly Cys Asn Lys Lys Phe Ala Gln Ser Thr Asn Leu
385 390 395 400
aaa tct cac atc tta aca cat gct aag gcc aaa aac aac cag 1482
Lys Ser His Ile Leu Thr His Ala Lys Ala Lys Asn Asn Gln
405 410
tgaaaagaag agagaagacc cttctcgacc acggaagca tcttcagaa gtgtgattgg 1542
gaataaataat gccctcctt tgtatattat ttctaggaag aattttaaaa atgaatccta 1602
cacacctaag ggacatgttt tgataaagta gtaaaaattt aaaaaaaaaa actttactaa 1662
gatgacattg ctaagatgct ctatcttgct ctgtaatctc gtttcaaaaa cacagtgttt 1722
ttgtaaagtg tggcccacac aggaggacaa ttcatgaact tcgcatcaaa agacaattct 1782
ttatacaaca gtgctaaaaa tgggacttct ttccacattc ttataaataat gaagctcacc 1842

tgttgcttac aatitititit aatitititit tccaagtgt gcatatigta cacitititig 1902
 gggatatgct tagtaatgct acgigtgatt tttctggagg ttgalaactt tgcitgcagt 1962
 agatititit taaaagaatg ggcagttaca tgcatacttc aaaagtatit tccigtatata 2022
 aaaaaaaaaag ttatataggt tttgtttgct atcttaatit tggttgtatit ctitgatgit 2082
 aacacatitit gtataatitgt atcgtatagc tgiattgaat catgtagtat caaatatitag 2142
 atgtgatitaa atagtgttaa tcaatttata cccattitag tcactititit tttccaaaaa 2202
 aatactgcca gatgctgatg ttcagtgtaa tttctitgcc tgitcagtta cagaaagtgg 2262
 tgcitcagtig tagaatgtat tgiacctit aacacctgat ggtacatcc catgtaacag 2322
 aaagggaac aataaaatag caatcctaaa g 2353

<210> 50

<211> 414

<212> PRT

<213> Homo sapiens

<400> 50

Met Ala Ser Gly Asp Thr Leu Tyr Ile Ala Thr Asp Gly Ser Glu Met

1 5 10 15

Pro Ala Glu Ile Val Glu Leu His Glu Ile Glu Val Glu Thr Ile Pro

20 25 30

Val Glu Thr Ile Glu Thr Thr Val Val Gly Glu Glu Glu Glu Asp

35 40 45

Asp Asp Asp Glu Asp Gly Gly Gly Gly Asp His Gly Gly Gly Gly Gly

50 55 60

His Gly His Ala Gly His His His His His His His His His His

65 70 75 80

Pro Pro Met Ile Ala Leu Gln Pro Leu Val Thr Asp Asp Pro Thr Gln

85 90 95

Val His His His Gln Glu Val Ile Leu Val Gln Thr Arg Glu Glu Val
 100 105 110
 Val Gly Gly Asp Asp Ser Asp Gly Leu Arg Ala Glu Asp Gly Phe Glu
 115 120 125
 Asp Gln Ile Leu Ile Pro Val Pro Ala Pro Ala Gly Gly Asp Asp Asp
 130 135 140
 Tyr Ile Glu Gln Thr Leu Val Thr Val Ala Ala Ala Gly Lys Ser Gly
 145 150 155 160
 Gly Gly Gly Ser Ser Ser Ser Gly Gly Gly Arg Val Lys Lys Gly Gly
 165 170 175
 Gly Lys Lys Ser Gly Lys Lys Ser Tyr Leu Ser Gly Gly Ala Gly Ala
 180 185 190
 Ala Gly Gly Arg Gly Ala Asp Pro Gly Asn Lys Lys Trp Glu Gln Lys
 195 200 205
 Gln Val Gln Ile Lys Thr Leu Glu Gly Glu Phe Ser Val Thr Met Trp
 210 215 220
 Ser Ser Asp Glu Lys Lys Asp Ile Asp His Glu Thr Val Val Glu Glu
 225 230 235 240
 Gln Ile Ile Gly Glu Asn Ser Pro Pro Asp Tyr Ser Glu Tyr Met Thr
 245 250 255
 Gly Lys Lys Leu Pro Pro Gly Gly Ile Pro Gly Ile Asp Leu Ser Asp
 260 265 270
 Pro Lys Gln Leu Ala Glu Phe Ala Arg Met Lys Pro Arg Lys Ile Lys
 275 280 285
 Glu Asp Asp Ala Pro Arg Thr Ile Ala Cys Pro His Lys Gly Cys Thr
 290 295 300

Lys Met Phe Arg Asp Asn Ser Ala Met Arg Lys His Leu His Thr His
305 310 315 320
Gly Pro Arg Val His Val Cys Ala Glu Cys Gly Lys Ala Phe Val Glu
325 330 335
Ser Ser Lys Leu Lys Arg His Gln Leu Val His Thr Gly Glu Lys Pro
340 345 350
Phe Gln Cys Thr Phe Glu Gly Cys Gly Lys Arg Phe Ser Leu Asp Phe
355 360 365
Asn Leu Arg Thr His Val Arg Ile His Thr Gly Asp Arg Pro Tyr Val
370 375 380
Cys Pro Phe Asp Gly Cys Asn Lys Lys Phe Ala Gln Ser Thr Asn Leu
385 390 395 400
Lys Ser His Ile Leu Thr His Ala Lys Ala Lys Asn Asn Gln
405 410

<210> 51

<211> 1229

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (222).. (950)

<400> 51

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gaagagactg gctccaggtc tgactcagtc cactacaagc tagacggctt tcttaaagca 120
ccaacattac ttgagtcitt ggataaaatt gagaaaagag tctacaagta ttgtggactc 180
tacaggaggc aggaggctga caactggcag taaagacaaa g atg tca ggc ctg cgg 236

										Met Ser Gly Leu Arg																				
										1					5															
ccc	ggc	act	caa	gtg	gac	cct	gag	att	gag	ctt	ttt	gta	aag	gct	gga	284														
Pro	Gly	Thr	Gln	Val	Asp	Pro	Glu	Ile	Glu	Leu	Phe	Val	Lys	Ala	Gly															
										10					15					20										
agt	gat	gga	gag	agt	att	gga	aac	tgt	ccc	ttt	tgc	caa	cgc	ctt	ttc	332														
Ser	Asp	Gly	Glu	Ser	Ile	Gly	Asn	Cys	Pro	Phe	Cys	Gln	Arg	Leu	Phe															
										25					30					35										
atg	atc	ctc	tgg	ctt	aaa	gga	gtt	aaa	ttt	aat	gtg	aca	act	gtt	gac	380														
Met	Ile	Leu	Trp	Leu	Lys	Gly	Val	Lys	Phe	Asn	Val	Thr	Thr	Val	Asp															
										40					45					50										
atg	acc	aga	aag	cct	gaa	gaa	cta	aag	gac	tta	gcc	cca	ggt	acc	aat	428														
Met	Thr	Arg	Lys	Pro	Glu	Glu	Leu	Lys	Asp	Leu	Ala	Pro	Gly	Thr	Asn															
										55					60					65										
cct	ccg	ttc	ctg	gtg	tat	aac	aag	gag	ttg	aaa	aca	gac	ttc	att	aaa	476														
Pro	Pro	Phe	Leu	Val	Tyr	Asn	Lys	Glu	Leu	Lys	Thr	Asp	Phe	Ile	Lys															
										70					75					80					85					
att	gag	gag	ttt	tta	gaa	caa	acc	ctg	gct	cct	cca	agg	tac	cct	cac	524														
Ile	Glu	Glu	Phe	Leu	Glu	Gln	Thr	Leu	Ala	Pro	Pro	Arg	Tyr	Pro	His															
										90					95					100										
ctg	agt	ccc	aag	tac	aag	gag	tct	ttt	gat	gtg	ggc	tgt	aac	ctc	ttt	572														
Leu	Ser	Pro	Lys	Tyr	Lys	Glu	Ser	Phe	Asp	Val	Gly	Cys	Asn	Leu	Phe															
										105					110					115										
gcc	aag	ttt	tct	gca	tac	att	aag	aat	aca	caa	aag	gag	gca	aat	aag	620														
Ala	Lys	Phe	Ser	Ala	Tyr	Ile	Lys	Asn	Thr	Gln	Lys	Glu	Ala	Asn	Lys															
										120					125					130										
aat	ttt	gaa	aaa	tct	ctg	ctc	aaa	gaa	ttc	aag	cgt	ctg	gat	gac	tac	668														

Asn Phe Glu Lys Ser Leu Leu Lys Glu Phe Lys Arg Leu Asp Asp Tyr
 135 140 145
 tta aac acc cca ctt ctg gat gaa att gat cca gac agt gct ggg gaa 716
 Leu Asn Thr Pro Leu Leu Asp Glu Ile Asp Pro Asp Ser Ala Gly Glu
 150 155 160 165
 ccc cca gtt tcc aga aga cta ttc ttg gat ggg gac cag cta aca ctg 764
 Pro Pro Val Ser Arg Arg Leu Phe Leu Asp Gly Asp Gln Leu Thr Leu
 170 175 180
 gct gat tgt agc ttg tta ccc aag ctg aac att att aaa gtt gct gcc 812
 Ala Asp Cys Ser Leu Leu Pro Lys Leu Asn Ile Ile Lys Val Ala Ala
 185 190 195
 aag aaa tat cgt gac ttt gac att cca gca gaa ttc tca gga gtc tgg 860
 Lys Lys Tyr Arg Asp Phe Asp Ile Pro Ala Glu Phe Ser Gly Val Trp
 200 205 210
 cgt tat ctc cac aat gcc tat gcc cgt gaa gaa ttt acc cac acg tgt 908
 Arg Tyr Leu His Asn Ala Tyr Ala Arg Glu Glu Phe Thr His Thr Cys
 215 220 225
 cct gaa gac aaa gaa att gaa aat act tac gca aat gtg gct 950
 Pro Glu Asp Lys Glu Ile Glu Asn Thr Tyr Ala Asn Val Ala
 230 235 240
 taaacagaag agttaggaga gctcttacag gagaaaaggc tatatttgtg atcagatttt 1010
 acttatlgac atattagaaa ggtttttgca aataagaata tgaaaaatac tgtttcttct 1070
 atccaactct cttatgaaaa ggaactctgt attttctatt agccataaat aatctgtcca 1130
 ctgtatttta caggcttcca tacttttact taattttctt tatctgtatg gcaaaccact 1190
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<211> 243

<212> PRT

<213> Homo sapiens

<400> 52

Met Ser Gly Leu Arg Pro Gly Thr Gln Val Asp Pro Glu Ile Glu Leu
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 20 25 30
 Cys Gln Arg Leu Phe Met Ile Leu Trp Leu Lys Gly Val Lys Phe Asn
 35 40 45
 Val Thr Thr Val Asp Met Thr Arg Lys Pro Glu Glu Leu Lys Asp Leu
 50 55 60
 Ala Pro Gly Thr Asn Pro Pro Phe Leu Val Tyr Asn Lys Glu Leu Lys
 65 70 75 80
 Thr Asp Phe Ile Lys Ile Glu Glu Phe Leu Glu Gln Thr Leu Ala Pro
 85 90 95
 Pro Arg Tyr Pro His Leu Ser Pro Lys Tyr Lys Glu Ser Phe Asp Val
 100 105 110
 Gly Cys Asn Leu Phe Ala Lys Phe Ser Ala Tyr Ile Lys Asn Thr Gln
 115 120 125
 Lys Glu Ala Asn Lys Asn Phe Glu Lys Ser Leu Leu Lys Glu Phe Lys
 130 135 140
 Arg Leu Asp Asp Tyr Leu Asn Thr Pro Leu Leu Asp Glu Ile Asp Pro
 145 150 155 160
 Asp Ser Ala Gly Glu Pro Pro Val Ser Arg Arg Leu Phe Leu Asp Gly
 165 170 175

Asp Gln Leu Thr Leu Ala Asp Cys Ser Leu Leu Pro Lys Leu Asn Ile

180

185

190

Ile Lys Val Ala Ala Lys Lys Tyr Arg Asp Phe Asp Ile Pro Ala Glu

195

200

205

Phe Ser Gly Val Trp Arg Tyr Leu His Asn Ala Tyr Ala Arg Glu Glu

210

215

220

Phe Thr His Thr Cys Pro Glu Asp Lys Glu Ile Glu Asn Thr Tyr Ala

225

230

235

240

Asn Val Ala

<210> 53

<211> 4001

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (2).. (316)

<400> 53

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Pro Gly Asn Pro Tyr Val Lys Val Asn Val Tyr Tyr Gly Arg Lys Arg

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15

att gcc aag aag aaa acc cat gtg aag aag tgc act ttg aac ccc atc 97

Ile Ala Lys Lys Lys Thr His Val Lys Lys Cys Thr Leu Asn Pro Ile

20

25

30

ttc aat gaa tct ttc atc tac gac atc ccc act gac ctc ctg cct gat 145

Phe Asn Glu Ser Phe Ile Tyr Asp Ile Pro Thr Asp Leu Leu Pro Asp

35

40

45

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 gag gtg gtg ggg agg ctg atc ctc ggg gca cac agt gtc aca gcc agt 241
 Glu Val Val Gly Arg Leu Ile Leu Gly Ala His Ser Val Thr Ala Ser
 65 70 75 80
 ggt gct gaa cac tgg aga gag gtc tgc gag agc ccc cgc aag cct gtg 289
 Gly Ala Glu His Trp Arg Glu Val Cys Glu Ser Pro Arg Lys Pro Val
 85 90 95
 gcc aag tgg cac agt ctg agc gag tac taatcctgtt cttctctcct 336
 Ala Lys Trp His Ser Leu Ser Glu Tyr
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<210> 54

<211> 105

<212> PRT

<213> Homo sapiens

<400> 54

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 Ile Ala Lys Lys Lys Thr His Val Lys Lys Cys Thr Leu Asn Pro Ile
 20 25 30
 Phe Asn Glu Ser Phe Ile Tyr Asp Ile Pro Thr Asp Leu Leu Pro Asp
 35 40 45
 Ile Ser Ile Glu Phe Leu Val Ile Asp Phe Asp Arg Thr Thr Lys Asn
 50 55 60
 Glu Val Val Gly Arg Leu Ile Leu Gly Ala His Ser Val Thr Ala Ser
 65 70 75 80
 Gly Ala Glu His Trp Arg Glu Val Cys Glu Ser Pro Arg Lys Pro Val
 85 90 95
 Ala Lys Trp His Ser Leu Ser Glu Tyr
 100 105

<210> 55

<211> 952

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (118).. (909)

<400> 55

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 atg gaa tca ggc ttc acc tcc aag gac acc tat cta agc cat ttt aac 165
 Met Glu Ser Gly Phe Thr Ser Lys Asp Thr Tyr Leu Ser His Phe Asn

1	5	10	15	
cct cgg gat tac cta gaa aaa tat tac aag ttt ggt tct agg cac tct	213			
Pro Arg Asp Tyr Leu Glu Lys Tyr Tyr Lys Phe Gly Ser Arg His Ser				
20	25	30		
gca gaa agc cag att ctt aag cac ctt ctg aaa aat ctt ttc aag ata	261			
Ala Glu Ser Gln Ile Leu Lys His Leu Leu Lys Asn Leu Phe Lys Ile				
35	40	45		
ttc tgc cta gac ggt gtg aag gga gac ctg ctg att gac atc ggc tct	309			
Phe Cys Leu Asp Gly Val Lys Gly Asp Leu Leu Ile Asp Ile Gly Ser				
50	55	60		
ggc ccc act atc tat cag ctc ctc tct gct tgt gaa tcc ttt aag gag	357			
Gly Pro Thr Ile Tyr Gln Leu Leu Ser Ala Cys Glu Ser Phe Lys Glu				
65	70	75	80	
atc gtc gtc act gac tac tca gac cag aac ctg cag gag ctg gag aag	405			
Ile Val Val Thr Asp Tyr Ser Asp Gln Asn Leu Gln Glu Leu Glu Lys				
85	90	95		
tgg ctg aag aaa gag cca gag gcc ttt gac tgg tcc cca gtg gtg acc	453			
Trp Leu Lys Lys Glu Pro Glu Ala Phe Asp Trp Ser Pro Val Val Thr				
100	105	110		
tat gtg tgt gat ctt gaa ggg aac aga gtc aag ggt cca gag aag gag	501			
Tyr Val Cys Asp Leu Glu Gly Asn Arg Val Lys Gly Pro Glu Lys Glu				
115	120	125		
gag aag ttg aga cag gcg gtc aag cag gtg ctg aag tgt gat gtg act	549			
Glu Lys Leu Arg Gln Ala Val Lys Gln Val Leu Lys Cys Asp Val Thr				
130	135	140		
cag agc cag cca ctg ggg gcc gtc ccc tta ccc ccg gct gac tgc gtg	597			
Gln Ser Gln Pro Leu Gly Ala Val Pro Leu Pro Pro Ala Asp Cys Val				

145	150	155	160	
ctc agc aca ctg tgt ctg gat gcc gcc tgc cca gac ctc ccc acc tac	645			
Leu Ser Thr Leu Cys Leu Asp Ala Ala Cys Pro Asp Leu Pro Thr Tyr				
165	170	175		
tgc agg gcg ctc agg aac ctc ggc agc cta ctg aag cca ggg ggc ttc	693			
Cys Arg Ala Leu Arg Asn Leu Gly Ser Leu Leu Lys Pro Gly Gly Phe				
180	185	190		
ctg gtg atc atg gat gcg ctc aag agc agc tac tac atg att ggt gag	741			
Leu Val Ile Met Asp Ala Leu Lys Ser Ser Tyr Tyr Met Ile Gly Glu				
195	200	205		
cag aag ttc tcc agc ctc ccc ctg ggc cgg gag gca gta gag gct gct	789			
Gln Lys Phe Ser Ser Leu Pro Leu Gly Arg Glu Ala Val Glu Ala Ala				
210	215	220		
gtg aaa gag gct ggc tac aca atc gaa tgg ttt gag gtg atc tcg caa	837			
Val Lys Glu Ala Gly Tyr Thr Ile Glu Trp Phe Glu Val Ile Ser Gln				
225	230	235	240	
agt tat tct tcc acc atg gcc aac aac gaa gga ctt ttc tcc ctg gtg	885			
Ser Tyr Ser Ser Thr Met Ala Asn Asn Glu Gly Leu Phe Ser Leu Val				
245	250	255		
gcg agg aag ctg agc aga ccc ctg tgatgcctgt gacctcaatt aaagcaattc	939			
Ala Arg Lys Leu Ser Arg Pro Leu				
260				
ctttgacctg tca				952

<210> 56

<211> 264

<212> PRT

<213> Homo sapiens

<400> 56

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Met Glu Ser Gly Phe Thr Ser Lys Asp Thr Tyr Leu Ser His Phe Asn
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Pro Arg Asp Tyr Leu Glu Lys Tyr Tyr Lys Phe Gly Ser Arg His Ser
      20             25             30
Ala Glu Ser Gln Ile Leu Lys His Leu Leu Lys Asn Leu Phe Lys Ile
      35             40             45
Phe Cys Leu Asp Gly Val Lys Gly Asp Leu Leu Ile Asp Ile Gly Ser
      50             55             60
Gly Pro Thr Ile Tyr Gln Leu Leu Ser Ala Cys Glu Ser Phe Lys Glu
      65             70             75             80
Ile Val Val Thr Asp Tyr Ser Asp Gln Asn Leu Gln Glu Leu Glu Lys
      85             90             95
Trp Leu Lys Lys Glu Pro Glu Ala Phe Asp Trp Ser Pro Val Val Thr
      100            105            110
Tyr Val Cys Asp Leu Glu Gly Asn Arg Val Lys Gly Pro Glu Lys Glu
      115            120            125
Glu Lys Leu Arg Gln Ala Val Lys Gln Val Leu Lys Cys Asp Val Thr
      130            135            140
Gln Ser Gln Pro Leu Gly Ala Val Pro Leu Pro Pro Ala Asp Cys Val
      145            150            155            160
Leu Ser Thr Leu Cys Leu Asp Ala Ala Cys Pro Asp Leu Pro Thr Tyr
      165            170            175
Cys Arg Ala Leu Arg Asn Leu Gly Ser Leu Leu Lys Pro Gly Gly Phe
      180            185            190

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Leu Val Ile Met Asp Ala Leu Lys Ser Ser Tyr Tyr Met Ile Gly Glu

195

200

205

Gln Lys Phe Ser Ser Leu Pro Leu Gly Arg Glu Ala Val Glu Ala Ala

210

215

220

Val Lys Glu Ala Gly Tyr Thr Ile Glu Trp Phe Glu Val Ile Ser Gln

225

230

235

240

Ser Tyr Ser Ser Thr Met Ala Asn Asn Glu Gly Leu Phe Ser Leu Val

245

250

255

Ala Arg Lys Leu Ser Arg Pro Leu

260

<210> 57

<211> 2617

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (94).. (633)

<400> 57

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cgcctccactg actgatagag cgaccggccg acc atg gcg ccc gga gtg gcc cgc 114

Met Ala Pro Gly Val Ala Arg

1

5

ggg ccg acg ccg tac tgg agg ttg cgc ctc ggt ggc gcc gcg ctg ctc 162

Gly Pro Thr Pro Tyr Trp Arg Leu Arg Leu Gly Gly Ala Ala Leu Leu

10

15

20

ctg ctg ctc atc ccg gtg gcc gcc gcg cag gag cct ccc gga gct gct 210

Leu Leu Leu Ile Pro Val Ala Ala Ala Gln Glu Pro Pro Gly Ala Ala
 25 30 35
 tgt tct cag aac aca aac aaa acc tgt gaa gag tgc ctg aag aac gtc 258
 Cys Ser Gln Asn Thr Asn Lys Thr Cys Glu Glu Cys Leu Lys Asn Val
 40 45 50 55
 tcc tgt ctt tgg tgc aac act aac aag gct tgt ctg gac tac cca gtt 306
 Ser Cys Leu Trp Cys Asn Thr Asn Lys Ala Cys Leu Asp Tyr Pro Val
 60 65 70
 aca agc gtc ttg cca ccg gct tcc ctt tgt aaa ttg agc tct gca cgc 354
 Thr Ser Val Leu Pro Pro Ala Ser Leu Cys Lys Leu Ser Ser Ala Arg
 75 80 85
 tgg gga gtt tgt tgg gtg aac ttt gag gcg ctg atc atc acc atg tgc 402
 Trp Gly Val Cys Trp Val Asn Phe Glu Ala Leu Ile Ile Thr Met Ser
 90 95 100
 gta gtc ggg gga acc ctc ctc ctg ggc att gcc atc tgc tgc tgc tgc 450
 Val Val Gly Gly Thr Leu Leu Leu Gly Ile Ala Ile Cys Cys Cys Cys
 105 110 115
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 Ala Met Arg Glu Arg Glu Glu Arg Arg Ile Arg Gln Glu Glu Arg Arg
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 Ala Glu Met Lys Thr Arg His Asp Glu Ile Arg Lys Lys Tyr Gly Leu
 155 160 165
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Phe Lys Glu Glu Asn Pro Tyr Ala Arg Phe Glu Asn Asn

170

175

180

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<210> 58

<211> 180

<212> PRT

<213> Homo sapiens

<400> 58

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Leu Gly Gly Ala Ala Leu Leu Leu Leu Ile Pro Val Ala Ala Ala

20 25 30

Gln Glu Pro Pro Gly Ala Ala Cys Ser Gln Asn Thr Asn Lys Thr Cys

35 40 45

Glu Glu Cys Leu Lys Asn Val Ser Cys Leu Trp Cys Asn Thr Asn Lys

50 55 60

Ala Cys Leu Asp Tyr Pro Val Thr Ser Val Leu Pro Pro Ala Ser Leu

65 70 75 80

Cys Lys Leu Ser Ser Ala Arg Trp Gly Val Cys Trp Val Asn Phe Glu

85 90 95

Ala Leu Ile Ile Thr Met Ser Val Val Gly Gly Thr Leu Leu Leu Gly

100

105

110

Ile Ala Ile Cys Cys Cys Cys Cys Cys Arg Arg Lys Arg Ser Arg Lys

115

120

125

Pro Asp Arg Ser Glu Glu Lys Ala Met Arg Glu Arg Glu Glu Arg Arg

130

135

140

Ile Arg Gln Glu Glu Arg Arg Ala Glu Met Lys Thr Arg His Asp Glu

145

150

155

160

Ile Arg Lys Lys Tyr Gly Leu Phe Lys Glu Glu Asn Pro Tyr Ala Arg

165

170

175

Phe Glu Asn Asn

180

<210> 59

<211> 3217

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (469).. (1875)

<400> 59

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cttttttctt ttttttgcatt ggcgctcttg gggctgttac acacacgcgc gctgtccatt 240
gcagcttaca taaaggcggg cgcgattatg caattatatt gtttagcata ttcaagagc 300
aatggctcgt tttcttagga ttcaacacg aaggcatcat gcatttttga aaaactagta 360

ttgagaataa taccttgcaa cgtaaagaat gtttttgggt atttttacac aatcictact 420

ttgaccaaac gagtcggac agttttcttt laattggaaaa taggagaa atg gag gaa 477

Met Glu Glu

1

aga atg gaa atg att tct gaa agg cca aaa gag agt atg tat tcc tgg 525

Arg Met Glu Met Ile Ser Glu Arg Pro Lys Glu Ser Met Tyr Ser Trp

5

10

15

aac aaa act gca gag aaa agt gat ttt gaa gct gta gaa gca ctt atg 573

Asn Lys Thr Ala Glu Lys Ser Asp Phe Glu Ala Val Glu Ala Leu Met

20

25

30

35

tca atg agc tgc agt tgg aag tct gat ttt aag aaa tac gtt gaa aac 621

Ser Met Ser Cys Ser Trp Lys Ser Asp Phe Lys Lys Tyr Val Glu Asn

40

45

50

aga cct gtt aca cca gta tct gat ttg tca gag gaa gag aat ctg ctt 669

Arg Pro Val Thr Pro Val Ser Asp Leu Ser Glu Glu Glu Asn Leu Leu

55

60

65

ccg gga aca cct gat ttt cat aca atc cca gca ttt tgt ttg act cca 717

Pro Gly Thr Pro Asp Phe His Thr Ile Pro Ala Phe Cys Leu Thr Pro

70

75

80

cct tac agt cct tct gac ttt gaa ccc tct caa gtg tca aat ctg atg 765

Pro Tyr Ser Pro Ser Asp Phe Glu Pro Ser Gln Val Ser Asn Leu Met

85

90

95

gca cca gcg cca tct act gta cac ttc aag tca ctc tca gat act gcc 813

Ala Pro Ala Pro Ser Thr Val His Phe Lys Ser Leu Ser Asp Thr Ala

100

105

110

115

aaa cct cac att gcc gca cct ttc aaa gag gaa gaa aag agc cca gta 861

Lys Pro His Ile Ala Ala Pro Phe Lys Glu Glu Glu Lys Ser Pro Val

120	125	130	
tct gcc ccc aaa ctc ccc aaa gct cag gca aca agt gtg att cgt cat	909		
Ser Ala Pro Lys Leu Pro Lys Ala Gln Ala Thr Ser Val Ile Arg His			
135	140	145	
aca gct gat gcc cag cta tgt aac cac cag acc tgc cca atg aaa gca	957		
Thr Ala Asp Ala Gln Leu Cys Asn His Gln Thr Cys Pro Met Lys Ala			
150	155	160	
gcc agc atc ctc aac tat cag aac aat tct ttt aga aga aga acc cac	1005		
Ala Ser Ile Leu Asn Tyr Gln Asn Asn Ser Phe Arg Arg Arg Thr His			
165	170	175	
cta aat gtt gag gct gca aga aag aac ata cca tgt gcc gct gtg tca	1053		
Leu Asn Val Glu Ala Ala Arg Lys Asn Ile Pro Cys Ala Ala Val Ser			
180	185	190	195
cca aac aga tcc aaa tgt gag aga aac aca gtg gca gat gtt gat gag	1101		
Pro Asn Arg Ser Lys Cys Glu Arg Asn Thr Val Ala Asp Val Asp Glu			
200	205	210	
aaa gca agt gct gca ctt tat gac ttt tct gtg cct tcc tca gag acg	1149		
Lys Ala Ser Ala Ala Leu Tyr Asp Phe Ser Val Pro Ser Ser Glu Thr			
215	220	225	
gtc atc tgc agg tct cag cca gcc cct gtg tcc cca caa cag aag tca	1197		
Val Ile Cys Arg Ser Gln Pro Ala Pro Val Ser Pro Gln Gln Lys Ser			
230	235	240	
gtg ttg gtc tct cca cct gca gta tct gca ggg gga gtg cca cct atg	1245		
Val Leu Val Ser Pro Pro Ala Val Ser Ala Gly Gly Val Pro Pro Met			
245	250	255	
ccg gtc atc tgc cag atg gtt ccc ctt cct gcc aac aac cct gtt gtg	1293		

Pro Val Ile Cys Gln Met Val Pro Leu Pro Ala Asn Asn Pro Val Val
 260 265 270 275
 aca aca gtc gtt ccc agc act cct ccc agc cag cca cca gct gtt tgc 1341
 Thr Thr Val Val Pro Ser Thr Pro Pro Ser Gln Pro Pro Ala Val Cys
 280 285 290
 ccc cct gtt gtg ttc atg ggc aca caa gtc ccc aaa ggc gct gtc atg 1389
 Pro Pro Val Val Phe Met Gly Thr Gln Val Pro Lys Gly Ala Val Met
 295 300 305
 ttt gtg gta ccc cag ccc gtt gtg cag agt tca aag cct ccg gtg gtg 1437
 Phe Val Val Pro Gln Pro Val Val Gln Ser Ser Lys Pro Pro Val Val
 310 315 320
 agc ccg aat ggc acc aga ctc tct ccc att gcc cct gct cct ggg ttt 1485
 Ser Pro Asn Gly Thr Arg Leu Ser Pro Ile Ala Pro Ala Pro Gly Phe
 325 330 335
 tcc cct tca gca gca aaa gtc act cct cag att gat tca tca agg ata 1533
 Ser Pro Ser Ala Ala Lys Val Thr Pro Gln Ile Asp Ser Ser Arg Ile
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 agg agt cac atc tgt agc cac cca gga tgt ggc aag aca tac ttt aaa 1581
 Arg Ser His Ile Cys Ser His Pro Gly Cys Gly Lys Thr Tyr Phe Lys
 360 365 370
 agt tcc cat ctg aag gcc cac acg agg acg cac aca gga gaa aag cct 1629
 Ser Ser His Leu Lys Ala His Thr Arg Thr His Thr Gly Glu Lys Pro
 375 380 385
 ttc agc tgt agc tgg aaa ggt tgt gaa agg agg ttt gcc cgt tct gat 1677
 Phe Ser Cys Ser Trp Lys Gly Cys Glu Arg Arg Phe Ala Arg Ser Asp
 390 395 400
 gaa ctg tcc aga cac agg cga acc cac acg ggt gag aag aaa ttt gcg 1725

Glu Leu Ser Arg His Arg Arg Thr His Thr Gly Glu Lys Lys Phe Ala
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 tgc ccc atg tgt gac cgg cgg ttc atg agg agt gac cat ttg acc aag 1773
 Cys Pro Met Cys Asp Arg Arg Phe Met Arg Ser Asp His Leu Thr Lys
 420 425 430 435
 cat gcc cgg cgc cat cta tca gcc aag aag cta cca aac tgg cag atg 1821
 His Ala Arg Arg His Leu Ser Ala Lys Lys Leu Pro Asn Trp Gln Met
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 Glu Val Ser Lys Leu Asn Asp Ile Ala Leu Pro Pro Thr Pro Ala Pro
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 aca cag tgacagaccg gaaagtgaag agtcagaact aactttgggc tcagcgggag 1925
 Thr Gln
 ccagtggtga tgtaaaaatg cttccactgc aagtcgtgtg cccacaacg tggcttaaag 1985
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<211> 469

<212> PRT

<213> Homo sapiens

<400> 60

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1	5	10	15
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Tyr Ser Trp Asn Lys Thr Ala Glu Lys Ser Asp Phe Glu Ala Val Glu

20	25	30
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Ala Leu Met Ser Met Ser Cys Ser Trp Lys Ser Asp Phe Lys Lys Tyr

35	40	45
----	----	----

Val Glu Asn Arg Pro Val Thr Pro Val Ser Asp Leu Ser Glu Glu Glu

50	55	60
----	----	----

Asn Leu Leu Pro Gly Thr Pro Asp Phe His Thr Ile Pro Ala Phe Cys

65	70	75	80
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Leu Thr Pro Pro Tyr Ser Pro Ser Asp Phe Glu Pro Ser Gln Val Ser

85	90	95
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Asn Leu Met Ala Pro Ala Pro Ser Thr Val His Phe Lys Ser Leu Ser
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Asp Thr Ala Lys Pro His Ile Ala Ala Pro Phe Lys Glu Glu Glu Lys
115 120 125
Ser Pro Val Ser Ala Pro Lys Leu Pro Lys Ala Gln Ala Thr Ser Val
130 135 140
Ile Arg His Thr Ala Asp Ala Gln Leu Cys Asn His Gln Thr Cys Pro
145 150 155 160
Met Lys Ala Ala Ser Ile Leu Asn Tyr Gln Asn Asn Ser Phe Arg Arg
165 170 175
Arg Thr His Leu Asn Val Glu Ala Ala Arg Lys Asn Ile Pro Cys Ala
180 185 190
Ala Val Ser Pro Asn Arg Ser Lys Cys Glu Arg Asn Thr Val Ala Asp
195 200 205
Val Asp Glu Lys Ala Ser Ala Ala Leu Tyr Asp Phe Ser Val Pro Ser
210 215 220
Ser Glu Thr Val Ile Cys Arg Ser Gln Pro Ala Pro Val Ser Pro Gln
225 230 235 240
Gln Lys Ser Val Leu Val Ser Pro Pro Ala Val Ser Ala Gly Gly Val
245 250 255
Pro Pro Met Pro Val Ile Cys Gln Met Val Pro Leu Pro Ala Asn Asn
260 265 270
Pro Val Val Thr Thr Val Val Pro Ser Thr Pro Pro Ser Gln Pro Pro
275 280 285
Ala Val Cys Pro Pro Val Val Phe Met Gly Thr Gln Val Pro Lys Gly
290 295 300
Ala Val Met Phe Val Val Pro Gln Pro Val Val Gln Ser Ser Lys Pro

305 310 315 320
Pro Val Val Ser Pro Asn Gly Thr Arg Leu Ser Pro Ile Ala Pro Ala
 325 330 335
Pro Gly Phe Ser Pro Ser Ala Ala Lys Val Thr Pro Gln Ile Asp Ser
 340 345 350
Ser Arg Ile Arg Ser His Ile Cys Ser His Pro Gly Cys Gly Lys Thr
 355 360 365
Tyr Phe Lys Ser Ser His Leu Lys Ala His Thr Arg Thr His Thr Gly
 370 375 380
Glu Lys Pro Phe Ser Cys Ser Trp Lys Gly Cys Glu Arg Arg Phe Ala
385 390 395 400
Arg Ser Asp Glu Leu Ser Arg His Arg Arg Thr His Thr Gly Glu Lys
 405 410 415
Lys Phe Ala Cys Pro Met Cys Asp Arg Arg Phe Met Arg Ser Asp His
 420 425 430
Leu Thr Lys His Ala Arg Arg His Leu Ser Ala Lys Lys Leu Pro Asn
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Trp Gln Met Glu Val Ser Lys Leu Asn Asp Ile Ala Leu Pro Pro Thr
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Pro Ala Pro Thr Gln
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<210> 61

<211> 1428

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (125).. (868)

<400> 61

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gcctcgccgt gcgctaggct tggagggaag gccigtctc gagtccgcgc ttctcgacac 120
cgcc atg tgc gga ggt ggt gtg att cgt ggc ccc gca ggg aac aac gat 169
      Met Ser Gly Gly Gly Val Ile Arg Gly Pro Ala Gly Asn Asn Asp
          1             5             10             15
tgc cgc atc tac glg ggt aac tta cct cca gac atc cga acc aag gac 217
Cys Arg Ile Tyr Val Gly Asn Leu Pro Pro Asp Ile Arg Thr Lys Asp
          20             25             30
att gag gac gtg ttc tac aaa tac ggc gct atc cgc gac atc gac ctg 265
Ile Glu Asp Val Phe Tyr Lys Tyr Gly Ala Ile Arg Asp Ile Asp Leu
          35             40             45
aag aat cgc cgc ggg gga ccg ccc ttc gcc ttc gtt gag ttc gag gac 313
Lys Asn Arg Arg Gly Gly Pro Pro Phe Ala Phe Val Glu Phe Glu Asp
          50             55             60
ccg cga gac gcg gaa gac gcg gtg tat ggt cgc gac ggc tat gat tac 361
Pro Arg Asp Ala Glu Asp Ala Val Tyr Gly Arg Asp Gly Tyr Asp Tyr
          65             70             75
gat ggg tac cgt ctg cgg glg gag ttt cct cga agc ggc cgt gga aca 409
Asp Gly Tyr Arg Leu Arg Val Glu Phe Pro Arg Ser Gly Arg Gly Thr
          80             85             90             95
ggc cga ggc ggc ggc ggg ggt gga ggt ggc gga gct ccc cga ggt cgc 457
Gly Arg Gly Gly Gly Gly Gly Gly Gly Gly Gly Ala Pro Arg Gly Arg
          100             105             110

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 Tyr Gly Pro Pro Ser Arg Arg Ser Glu Asn Arg Val Val Val Ser Gly
 115 120 125
 ctg cct cca agt gga agt tgg cag gat tta aag gat cac atg cgt gaa 553
 Leu Pro Pro Ser Gly Ser Trp Gln Asp Leu Lys Asp His Met Arg Glu
 130 135 140
 gca ggt gat gla tgt tat gct gat gtt tac cga gat ggc act ggt gtc 601
 Ala Gly Asp Val Cys Tyr Ala Asp Val Tyr Arg Asp Gly Thr Gly Val
 145 150 155
 gtg gag ttt gla cgg aaa gaa gat atg acc tat gca gtt cga aaa ctg 649
 Val Glu Phe Val Arg Lys Glu Asp Met Thr Tyr Ala Val Arg Lys Leu
 160 165 170 175
 gat aac act aag ttt aga tct cat gag gga gaa act gcc tac atc cgg 697
 Asp Asn Thr Lys Phe Arg Ser His Glu Gly Glu Thr Ala Tyr Ile Arg
 180 185 190
 gtt aaa gtt gat ggg ccc aga agt cca agt tat gga aga tct cga tct 745
 Val Lys Val Asp Gly Pro Arg Ser Pro Ser Tyr Gly Arg Ser Arg Ser
 195 200 205
 cga agc cgt agt cgt agc aga agc cgt agc aga agc aac agc agg agt 793
 Arg Ser Arg Ser Arg Ser Arg Ser Arg Ser Arg Ser Asn Ser Arg Ser
 210 215 220
 cgc agt tac tcc cca agg aga agc aga gga tca cca cgc tat tct ccc 841
 Arg Ser Tyr Ser Pro Arg Arg Ser Arg Gly Ser Pro Arg Tyr Ser Pro
 225 230 235
 cgt cat agc aga tct cgc tct cgt aca taagatgatt ggtgacactt 888
 Arg His Ser Arg Ser Arg Ser Arg Thr
 240 245

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<210> 62

<211> 248

<212> PRT

<213> Homo sapiens

<400> 62

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Arg Ile Tyr Val Gly Asn Leu Pro Pro Asp Ile Arg Thr Lys Asp Ile

20 25 30

Glu Asp Val Phe Tyr Lys Tyr Gly Ala Ile Arg Asp Ile Asp Leu Lys

35 40 45

Asn Arg Arg Gly Gly Pro Pro Phe Ala Phe Val Glu Phe Glu Asp Pro

50 55 60

Arg Asp Ala Glu Asp Ala Val Tyr Gly Arg Asp Gly Tyr Asp Tyr Asp

65 70 75 80

Gly Tyr Arg Leu Arg Val Glu Phe Pro Arg Ser Gly Arg Gly Thr Gly

85 90 95

Arg Gly Gly Gly Gly Gly Gly Gly Gly Gly Ala Pro Arg Gly Arg Tyr
100 105 110
Gly Pro Pro Ser Arg Arg Ser Glu Asn Arg Val Val Val Ser Gly Leu
115 120 125
Pro Pro Ser Gly Ser Trp Gln Asp Leu Lys Asp His Met Arg Glu Ala
130 135 140
Gly Asp Val Cys Tyr Ala Asp Val Tyr Arg Asp Gly Thr Gly Val Val
145 150 155 160
Glu Phe Val Arg Lys Glu Asp Met Thr Tyr Ala Val Arg Lys Leu Asp
165 170 175
Asn Thr Lys Phe Arg Ser His Glu Gly Glu Thr Ala Tyr Ile Arg Val
180 185 190
Lys Val Asp Gly Pro Arg Ser Pro Ser Tyr Gly Arg Ser Arg Ser Arg
195 200 205
Ser Arg Ser Arg Ser Arg Ser Arg Ser Arg Ser Asn Ser Arg Ser Arg
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Ser Tyr Ser Pro Arg Arg Ser Arg Gly Ser Pro Arg Tyr Ser Pro Arg
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<210> 63

<211> 3664

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (195).. (1943)

<400> 63

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acccctgcc tggccccctt gcccaactg gcaggggggc caggctgggc agcagccccct 180
ctttcacctc aact atg gat ctc ctg ccc ccc aag ccc aag tac aat cca 230

      Met Asp Leu Leu Pro Pro Lys Pro Lys Tyr Asn Pro
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ctc cgg aat gag tct ctg tca tcg ctg gag gaa ggg gct tct ggg tcc 278
Leu Arg Asn Glu Ser Leu Ser Ser Leu Glu Glu Gly Ala Ser Gly Ser
            15              20              25

acc ccc ccg gag gag ctg cct tcc cca tca gct tca tcc ctg ggg ccc 326
Thr Pro Pro Glu Glu Leu Pro Ser Pro Ser Ala Ser Ser Leu Gly Pro
            30              35              40

atc ctg cct cct ctg cct ggg gac gat agt ccc act acc ctg tgc tcc 374
Ile Leu Pro Pro Leu Pro Gly Asp Asp Ser Pro Thr Thr Leu Cys Ser
            45              50              55              60

ttc ttc ccc cgg atg agc aac ctg agg ctg gcc aac ccg gct ggg ggg 422
Phe Phe Pro Arg Met Ser Asn Leu Arg Leu Ala Asn Pro Ala Gly Gly
            65              70              75

cgc cca ggg tct aag ggg gag cca gga agg gca gct gat gat ggg gag 470
Arg Pro Gly Ser Lys Gly Glu Pro Gly Arg Ala Ala Asp Asp Gly Glu
            80              85              90

ggg atc gat ggg gca gcc atg cca gag tca ggc ccc cta ccc ctc ctc 518
Gly Ile Asp Gly Ala Ala Met Pro Glu Ser Gly Pro Leu Pro Leu Leu
            95              100              105

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 Gln Asp Met Asn Lys Leu Ser Gly Gly Gly Gly Arg Arg Thr Arg Val
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 Glu Gly Gly Gln Leu Gly Gly Glu Glu Trp Thr Arg His Gly Ser Phe
 125 130 135 140
 gtc aat aag ccc acg cgg ggc tgg ctg cat ccc aac gac aaa gtc atg 662
 Val Asn Lys Pro Thr Arg Gly Trp Leu His Pro Asn Asp Lys Val Met
 145 150 155
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 Gly Pro Gly Val Ser Tyr Leu Val Arg Tyr Met Gly Cys Val Glu Val
 160 165 170
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 Leu Gln Ser Met Arg Ala Leu Asp Phe Asn Thr Arg Thr Gln Val Thr
 175 180 185
 agg gag gcc atc agt ctg gtg tgt gag gct gtg ccg ggt gct aag ggg 806
 Arg Glu Ala Ile Ser Leu Val Cys Glu Ala Val Pro Gly Ala Lys Gly
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 Ala Thr Arg Arg Arg Lys Pro Cys Ser Arg Pro Leu Ser Ser Ile Leu
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 ggg agg agt aac ctg aaa ttt gct gga atg cca atc act ctc acc gtc 902
 Gly Arg Ser Asn Leu Lys Phe Ala Gly Met Pro Ile Thr Leu Thr Val
 225 230 235
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 Ser Thr Ser Ser Leu Asn Leu Met Ala Ala Asp Cys Lys Gln Ile Ile
 240 245 250

gcc aac cac cac atg caa tct atc tca ttt gca tcc ggc ggg gat ccg 998
 Ala Asn His His Met Gln Ser Ile Ser Phe Ala Ser Gly Gly Asp Pro
 255 260 265
 gac aca gcc gag tat gtc gcc tat gtt gcc aaa gac cct gtg aat cag 1046
 Asp Thr Ala Glu Tyr Val Ala Tyr Val Ala Lys Asp Pro Val Asn Gln
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 aga gcc tgc cac att ctg gag tgt ccc gaa ggg ctt gcc cag gat gtc 1094
 Arg Ala Cys His Ile Leu Glu Cys Pro Glu Gly Leu Ala Gln Asp Val
 285 290 295 300
 atc agc acc att ggc cag gcc ttc gag ttg cgc ttc aaa caa tac ctc 1142
 Ile Ser Thr Ile Gly Gln Ala Phe Glu Leu Arg Phe Lys Gln Tyr Leu
 305 310 315
 agg aac cca ccc aaa ctg gtc acc cct cat gac agg atg gct ggc ttt 1190
 Arg Asn Pro Pro Lys Leu Val Thr Pro His Asp Arg Met Ala Gly Phe
 320 325 330
 gat ggc tca gca tgg gat gag gag gag gaa gag cca cct gac cat cag 1238
 Asp Gly Ser Ala Trp Asp Glu Glu Glu Glu Glu Pro Pro Asp His Gln
 335 340 345
 tac tat aat gac ttc ccg ggg aag gaa ccc ccc ttg ggg ggg gtg gta 1286
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 gac atg agg ctt cgg gaa gga gcc gct cca ggg gct gct cga ccc act 1334
 Asp Met Arg Leu Arg Glu Gly Ala Ala Pro Gly Ala Ala Arg Pro Thr
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 gca ccc aat gcc cag acc ccc agc cac ttg gga gct aca ttg cct gta 1382
 Ala Pro Asn Ala Gln Thr Pro Ser His Leu Gly Ala Thr Leu Pro Val

385	390	395	
gga cag cct gtt ggg gga gat cca gaa gtc cgc aaa cag atg cca cct	1430		
Gly Gln Pro Val Gly Gly Asp Pro Glu Val Arg Lys Gln Met Pro Pro			
400	405	410	
cca cca ccc tgt cca ggc aga gag ctt ttt gat gat ccc tcc tat gtc	1478		
Pro Pro Pro Cys Pro Gly Arg Glu Leu Phe Asp Asp Pro Ser Tyr Val			
415	420	425	
aac gtc cag aac cta gac aag gcc cgg caa gca gtg ggt ggt gct ggg	1526		
Asn Val Gln Asn Leu Asp Lys Ala Arg Gln Ala Val Gly Gly Ala Gly			
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445	450	455	460
atg aag ccc ttc gaa gat gct ctt cgg gtg cct cca cct ccc cag tcg	1622		
Met Lys Pro Phe Glu Asp Ala Leu Arg Val Pro Pro Pro Pro Gln Ser			
465	470	475	
gtg tcc atg gct gag cag ctc cga ggg gag ccc tgg ttc cat ggg aag	1670		
Val Ser Met Ala Glu Gln Leu Arg Gly Glu Pro Trp Phe His Gly Lys			
480	485	490	
ctg agc cgg cgg gag gct gag gca ctg ctg cag ctc aat ggg gac ttc	1718		
Leu Ser Arg Arg Glu Ala Glu Ala Leu Leu Gln Leu Asn Gly Asp Phe			
495	500	505	
tig gta cgg gag agc acg acc aca cct ggc cag tat gtg ctc act ggc	1766		
Leu Val Arg Glu Ser Thr Thr Thr Pro Gly Gln Tyr Val Leu Thr Gly			
510	515	520	
tig cag agt ggg cag cct aag cat ttg cta ctg gtg gac cct gag ggt	1814		
Leu Gln Ser Gly Gln Pro Lys His Leu Leu Leu Val Asp Pro Glu Gly			

525 530 535 540
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 Val Val Arg Thr Lys Asp His Arg Phe Glu Ser Val Ser His Leu Ile
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 agc tac cac atg gac aat cac ttg ccc atc atc tct gcg ggc agc gaa 1910
 Ser Tyr His Met Asp Asn His Leu Pro Ile Ile Ser Ala Gly Ser Glu
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 Leu Cys Leu Gln Gln Pro Val Glu Arg Lys Leu
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<210> 64

<211> 583

<212> PRT

<213> Homo sapiens

<400> 64

Met Asp Leu Leu Pro Pro Lys Pro Lys Tyr Asn Pro Leu Arg Asn Glu

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Ser Leu Ser Ser Leu Glu Glu Gly Ala Ser Gly Ser Thr Pro Pro Glu

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Glu Leu Pro Ser Pro Ser Ala Ser Ser Leu Gly Pro Ile Leu Pro Pro

35 40 45

Leu Pro Gly Asp Asp Ser Pro Thr Thr Leu Cys Ser Phe Phe Pro Arg

50 55 60

WO 01/25427

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 65 70 75 80
 Lys Gly Glu Pro Gly Arg Ala Ala Asp Asp Gly Glu Gly Ile Asp Gly
 85 90 95
 Ala Ala Met Pro Glu Ser Gly Pro Leu Pro Leu Leu Gln Asp Met Asn
 100 105 110
 Lys Leu Ser Gly Gly Gly Gly Arg Arg Thr Arg Val Glu Gly Gly Gln
 115 120 125
 Leu Gly Gly Glu Glu Trp Thr Arg His Gly Ser Phe Val Asn Lys Pro
 130 135 140
 Thr Arg Gly Trp Leu His Pro Asn Asp Lys Val Met Gly Pro Gly Val
 145 150 155 160
 Ser Tyr Leu Val Arg Tyr Met Gly Cys Val Glu Val Leu Gln Ser Met
 165 170 175
 Arg Ala Leu Asp Phe Asn Thr Arg Thr Gln Val Thr Arg Glu Ala Ile
 180 185 190
 Ser Leu Val Cys Glu Ala Val Pro Gly Ala Lys Gly Ala Thr Arg Arg
 195 200 205
 Arg Lys Pro Cys Ser Arg Pro Leu Ser Ser Ile Leu Gly Arg Ser Asn
 210 215 220
 Leu Lys Phe Ala Gly Met Pro Ile Thr Leu Thr Val Ser Thr Ser Ser
 225 230 235 240
 Leu Asn Leu Met Ala Ala Asp Cys Lys Gln Ile Ile Ala Asn His His
 245 250 255
 Met Gln Ser Ile Ser Phe Ala Ser Gly Gly Asp Pro Asp Thr Ala Glu
 260 265 270
 Tyr Val Ala Tyr Val Ala Lys Asp Pro Val Asn Gln Arg Ala Cys His

275	280	285	
Ile Leu Glu Cys Pro Glu Gly Leu Ala Gln Asp Val Ile Ser Thr Ile			
290	295	300	
Gly Gln Ala Phe Glu Leu Arg Phe Lys Gln Tyr Leu Arg Asn Pro Pro			
305	310	315	320
Lys Leu Val Thr Pro His Asp Arg Met Ala Gly Phe Asp Gly Ser Ala			
325	330	335	
Trp Asp Glu Glu Glu Glu Glu Pro Pro Asp His Gln Tyr Tyr Asn Asp			
340	345	350	
Phe Pro Gly Lys Glu Pro Pro Leu Gly Gly Val Val Asp Met Arg Leu			
355	360	365	
Arg Glu Gly Ala Ala Pro Gly Ala Ala Arg Pro Thr Ala Pro Asn Ala			
370	375	380	
Gln Thr Pro Ser His Leu Gly Ala Thr Leu Pro Val Gly Gln Pro Val			
385	390	395	400
Gly Gly Asp Pro Glu Val Arg Lys Gln Met Pro Pro Pro Pro Pro Cys			
405	410	415	
Pro Gly Arg Glu Leu Phe Asp Asp Pro Ser Tyr Val Asn Val Gln Asn			
420	425	430	
Leu Asp Lys Ala Arg Gln Ala Val Gly Gly Ala Gly Pro Pro Asn Pro			
435	440	445	
Ala Ile Asn Gly Ser Ala Pro Arg Asp Leu Phe Asp Met Lys Pro Phe			
450	455	460	
Glu Asp Ala Leu Arg Val Pro Pro Pro Pro Gln Ser Val Ser Met Ala			
465	470	475	480
Glu Gln Leu Arg Gly Glu Pro Trp Phe His Gly Lys Leu Ser Arg Arg			

485 490 495
 Glu Ala Glu Ala Leu Leu Gln Leu Asn Gly Asp Phe Leu Val Arg Glu
 500 505 510
 Ser Thr Thr Thr Pro Gly Gln Tyr Val Leu Thr Gly Leu Gln Ser Gly
 515 520 525
 Gln Pro Lys His Leu Leu Leu Val Asp Pro Glu Gly Val Val Arg Thr
 530 535 540
 Lys Asp His Arg Phe Glu Ser Val Ser His Leu Ile Ser Tyr His Met
 545 550 555 560
 Asp Asn His Leu Pro Ile Ile Ser Ala Gly Ser Glu Leu Cys Leu Gln
 565 570 575
 Gln Pro Val Glu Arg Lys Leu
 580

<210> 65

<211> 2493

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (41).. (1237)

<400> 65

actgcgactc gagacagcgg cccggcagga cagctccaga atg aaa atg cgg ttc 55

Met Lys Met Arg Phe

1 5

ttg ggg ttg gtg gtc tgt ttg gtt ctc tgg ccc ctg cat tct gag ggg 103

Leu Gly Leu Val Val Cys Leu Val Leu Trp Pro Leu His Ser Glu Gly

10	15	20	
tct gga ggg aaa ctg aca gct gtg gat cct gaa aca aac atg aat gtg	151		
Ser Gly Gly Lys Leu Thr Ala Val Asp Pro Glu Thr Asn Met Asn Val			
25	30	35	
agt gaa att atc tct tac tgg gga ttc cct agt gag gaa tac cta gtt	199		
Ser Glu Ile Ile Ser Tyr Trp Gly Phe Pro Ser Glu Glu Tyr Leu Val			
40	45	50	
gag aca gaa gat gga tat att ctg tgc ctt aac cga att cct cat ggg	247		
Glu Thr Glu Asp Gly Tyr Ile Leu Cys Leu Asn Arg Ile Pro His Gly			
55	60	65	
agg aag aac cat tct gac aaa ggt ccc aaa cca gtt gtc ttc ctg caa	295		
Arg Lys Asn His Ser Asp Lys Gly Pro Lys Pro Val Val Phe Leu Gln			
70	75	80	85
cat ggc ttg ctg gca gat tct agt aac tgg gtc aca aac ctt gcc aac	343		
His Gly Leu Leu Ala Asp Ser Ser Asn Trp Val Thr Asn Leu Ala Asn			
90	95	100	
agc agc ctg ggc ttc att ctt gct gat gct ggt ttt gac gtg tgg atg	391		
Ser Ser Leu Gly Phe Ile Leu Ala Asp Ala Gly Phe Asp Val Trp Met			
105	110	115	
ggc aac agc aga gga aat acc tgg tct cgg aaa cat aag aca ctc tca	439		
Gly Asn Ser Arg Gly Asn Thr Trp Ser Arg Lys His Lys Thr Leu Ser			
120	125	130	
gtt tct cag gat gaa ttc tgg gct ttc agt tat gat gag atg gca aaa	487		
Val Ser Gln Asp Glu Phe Trp Ala Phe Ser Tyr Asp Glu Met Ala Lys			
135	140	145	
tat gac cta cca gct tcc att aac ttc att ctg aat aaa act ggc caa	535		
Tyr Asp Leu Pro Ala Ser Ile Asn Phe Ile Leu Asn Lys Thr Gly Gln			

150	155	160	165	
gaa caa gtg tat tat gtg ggt cat tct caa ggc acc act ala ggt ttt				583
Glu Gln Val Tyr Tyr Val Gly His Ser Gln Gly Thr Thr Ile Gly Phe				
	170	175	180	
ata gca ttt tca cag atc cct gag ctg gct aaa agg att aaa atg ttt				631
Ile Ala Phe Ser Gln Ile Pro Glu Leu Ala Lys Arg Ile Lys Met Phe				
	185	190	195	
ttt gcc ctg ggt cct gtg gct tcc gtc gcc ttc tgt act agc cct atg				679
Phe Ala Leu Gly Pro Val Ala Ser Val Ala Phe Cys Thr Ser Pro Met				
	200	205	210	
gcc aaa tta gga cga tta cca gat cat ctc att aag gac tta ttt gga				727
Ala Lys Leu Gly Arg Leu Pro Asp His Leu Ile Lys Asp Leu Phe Gly				
	215	220	225	
gac aaa gaa ttt ctt ccc cag agt gcg ttt ttg aag tgg ctg ggt acc				775
Asp Lys Glu Phe Leu Pro Gln Ser Ala Phe Leu Lys Trp Leu Gly Thr				
230	235	240	245	
cac gtt tgc act cat gtc ata ctg aag gag ctc tgt gga aat ctc tgt				823
His Val Cys Thr His Val Ile Leu Lys Glu Leu Cys Gly Asn Leu Cys				
	250	255	260	
ttt ctt ctg tgt gga ttt aat gag aga aat tta aat atg tct aga gtg				871
Phe Leu Leu Cys Gly Phe Asn Glu Arg Asn Leu Asn Met Ser Arg Val				
	265	270	275	
gat gta tat aca aca cat tct cct gct gga act tct gtg caa aac atg				919
Asp Val Tyr Thr Thr His Ser Pro Ala Gly Thr Ser Val Gln Asn Met				
	280	285	290	
tta cac tgg agc cag gct gtt aaa ttc caa aag ttt caa gcc ttt gac				967

Leu His Trp Ser Gln Ala Val Lys Phe Gln Lys Phe Gln Ala Phe Asp
 295 300 305
 tgg gga agc agt gcc aag aat tat ttt cat tac aac cag agt tat cct 1015
 Trp Gly Ser Ser Ala Lys Asn Tyr Phe His Tyr Asn Gln Ser Tyr Pro
 310 315 320 325
 ccc aca tac aat gtg aag gac atg ctt gtg ccg act gca gtc tgg agc 1063
 Pro Thr Tyr Asn Val Lys Asp Met Leu Val Pro Thr Ala Val Trp Ser
 330 335 340
 ggg ggt cac gac tgg ctt gca gat gtc tac gac gtc aat atc tta ctg 1111
 Gly Gly His Asp Trp Leu Ala Asp Val Tyr Asp Val Asn Ile Leu Leu
 345 350 355
 act cag atc acc aac ttg gtg ttc cat gag agc att ccg gaa tgg gag 1159
 Thr Gln Ile Thr Asn Leu Val Phe His Glu Ser Ile Pro Glu Trp Glu
 360 365 370
 cat ctt gac ttc att tgg ggc ctg gat gcc cct tgg agg ctt tat aat 1207
 His Leu Asp Phe Ile Trp Gly Leu Asp Ala Pro Trp Arg Leu Tyr Asn
 375 380 385
 aaa att att aat cta atg agg aaa tat cag tgaaagctgg acttgagctg 1257
 Lys Ile Ile Asn Leu Met Arg Lys Tyr Gln
 390 395
 tgtaccacca agtcaatgat tatgtcatgt gaaaatgtgt ttgcttcatt tctgtaaaac 1317
 acttgltttt ctttcccagg tcttttgttt ttttataacc aagaaaatga taactttgaa 1377
 gatgccagct tcactctagt ttcaattaga aacatactag ctattttttc ttttaattagg 1437
 gctggaatag gaagccagtg tcicaacat agtatgtct ctttaagtct tttaaatc 1497
 actgaigtgt aaaaaggica ttatatccat tctgttttta aaatttaaaa tatattgact 1557
 ttttgccctt cataggacaa agtaatatat ggttggaat tttaaaattg tgttgctcatt 1617
 ggtaaatctg tcactgactt aagcgaggta taaaagiacc cagttttcat gtccttgcc 1677

taaagagctc tctagctcaa cggctcttga gttagagatc taaatgacat ttatcatgt 1737
 tttccctgcag caggctcata gtcaaatcca gaaatacac agctgtgcc aataaagga 1797
 tgctaacaat taattttatc aaacctaaat gtgacagcig tgatttgaca cgttttaatt 1857
 gctcaggtaa aatgaaatag tttccggcgg tcttcaaaaa caaatgcac tgataaaaca 1917
 aaaacaaaag tatgttttaa atgctttgaa gactgataca ctcaaccatc tataatcatg 1977
 agctctcaat ttcatggcag gccatagttc tacitattcg agaagcaaat cctgtggag 2037
 actataccac tattttttct gagattaatg tactcttggg gcccgctact gtcgttattg 2097
 atcacatcig tctgaagcca aagccccgtg gtgccccatg agaagtgtcc ttgttcattt 2157
 tcacccaaat gaagtgtgaa cgtgatgttt tcggatgcaa actcagctca gggattcatt 2217
 ttgtgtctta gttttataig catccttatt tttaatcac ctgcttcacg tccctatgtt 2277
 gggaagtcca tatttgtctg ctttcttgc agcatcattt ccttacaata ctgtccggtg 2337
 gacaaaatga caattgatat gttttctga tataattact ttagctgcac taacagtaca 2397
 atgcttgtaa atggttaata taggcagggc gaatactact ttgttaacttt taaagtctta 2457
 aacttttcaa taaaattgag tgagacttat aggcc 2493

<210> 66

<211> 399

<212> PRT

<213> Homo sapiens

<400> 66

Met Lys Met Arg Phe Leu Gly Leu Val Val Cys Leu Val Leu Trp Pro

1

5

10

15

Leu His Ser Glu Gly Ser Gly Gly Lys Leu Thr Ala Val Asp Pro Glu

20

25

30

Thr Asn Met Asn Val Ser Glu Ile Ile Ser Tyr Trp Gly Phe Pro Ser

35

40

45

Glu Glu Tyr Leu Val Glu Thr Glu Asp Gly Tyr Ile Leu Cys Leu Asn

50	55	60	
Arg Ile Pro His Gly Arg Lys Asn His Ser Asp Lys Gly Pro Lys Pro			
65	70	75	80
Val Val Phe Leu Gln His Gly Leu Leu Ala Asp Ser Ser Asn Trp Val			
85	90	95	
Thr Asn Leu Ala Asn Ser Ser Leu Gly Phe Ile Leu Ala Asp Ala Gly			
100	105	110	
Phe Asp Val Trp Met Gly Asn Ser Arg Gly Asn Thr Trp Ser Arg Lys			
115	120	125	
His Lys Thr Leu Ser Val Ser Gln Asp Glu Phe Trp Ala Phe Ser Tyr			
130	135	140	
Asp Glu Met Ala Lys Tyr Asp Leu Pro Ala Ser Ile Asn Phe Ile Leu			
145	150	155	160
Asn Lys Thr Gly Gln Glu Gln Val Tyr Tyr Val Gly His Ser Gln Gly			
165	170	175	
Thr Thr Ile Gly Phe Ile Ala Phe Ser Gln Ile Pro Glu Leu Ala Lys			
180	185	190	
Arg Ile Lys Met Phe Phe Ala Leu Gly Pro Val Ala Ser Val Ala Phe			
195	200	205	
Cys Thr Ser Pro Met Ala Lys Leu Gly Arg Leu Pro Asp His Leu Ile			
210	215	220	
Lys Asp Leu Phe Gly Asp Lys Glu Phe Leu Pro Gln Ser Ala Phe Leu			
225	230	235	240
Lys Trp Leu Gly Thr His Val Cys Thr His Val Ile Leu Lys Glu Leu			
245	250	255	
Cys Gly Asn Leu Cys Phe Leu Leu Cys Gly Phe Asn Glu Arg Asn Leu			

260 265 270
Asn Met Ser Arg Val Asp Val Tyr Thr Thr His Ser Pro Ala Gly Thr
275 280 285
Ser Val Gln Asn Met Leu His Trp Ser Gln Ala Val Lys Phe Gln Lys
290 295 300
Phe Gln Ala Phe Asp Trp Gly Ser Ser Ala Lys Asn Tyr Phe His Tyr
305 310 315 320
Asn Gln Ser Tyr Pro Pro Thr Tyr Asn Val Lys Asp Met Leu Val Pro
325 330 335
Thr Ala Val Trp Ser Gly Gly His Asp Trp Leu Ala Asp Val Tyr Asp
340 345 350
Val Asn Ile Leu Leu Thr Gln Ile Thr Asn Leu Val Phe His Glu Ser
355 360 365
Ile Pro Glu Trp Glu His Leu Asp Phe Ile Trp Gly Leu Asp Ala Pro
370 375 380
Trp Arg Leu Tyr Asn Lys Ile Ile Asn Leu Met Arg Lys Tyr Gln
385 390 395

<210> 67

<211> 1633

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (323).. (1177)

<400> 67

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cattaatga cagctgaccc aggtgctaca cagaagtgga ttcagtgaat cttaggaagac 120
 agcagcagac aggatccag gaaccaggtt ttgatgaagc taggactgag gagcaagcga 180
 gcaagcagca gttcgtggaa tctgtctgc tgcgtcttc ctggtttagg agccgacggg 240
 cgctcgcagg ctacgcgcgc gctgccgcgc gcaggacccg gccgcctccg ccgccgccgc 300
 cgcccctaag cctcccgaag cc atg gcc ggg ctc ggc cac ccc gcc gcc ttc 352

Met Ala Gly Leu Gly His Pro Ala Ala Phe

1 5 10

ggc cgg gcc acc cac gcc gtg gtg cgg gcg cta ccc gag tcg ctc ggc 400
 Gly Arg Ala Thr His Ala Val Val Arg Ala Leu Pro Glu Ser Leu Gly

15 20 25

cag cac gcg ctg aga agc gcc aag ggc gag gag gtg gac gtc gcc cgc 448
 Gln His Ala Leu Arg Ser Ala Lys Gly Glu Glu Val Asp Val Ala Arg

30 35 40

gcg gaa cgg cag cac cag ctc tac gtg ggc glg ctg ggc agc aag ctg 496
 Ala Glu Arg Gln His Gln Leu Tyr Val Gly Val Leu Gly Ser Lys Leu

45 50 55

ggg ctg cag gtg gtg gag ctg ccg gcc gac gag agc ctt ccg gac tgc 544
 Gly Leu Gln Val Val Glu Leu Pro Ala Asp Glu Ser Leu Pro Asp Cys

60 65 70

gtc ttc gtg gag gac gtg gcc glg gtg tgc gag gag acg gcc ctc atc 592
 Val Phe Val Glu Asp Val Ala Val Val Cys Glu Glu Thr Ala Leu Ile

75 80 85 90

acc cga ccc ggg gcg ccg agc cgg agg aag gag gtt gac atg atg aaa 640
 Thr Arg Pro Gly Ala Pro Ser Arg Arg Lys Glu Val Asp Met Met Lys

95 100 105

gaa gca tta gaa aaa ctt cag ctc aat ata gta gag atg aaa gat gaa 688
 Glu Ala Leu Glu Lys Leu Gln Leu Asn Ile Val Glu Met Lys Asp Glu

110	115	120	
aat gca act tta gat ggc gga gat gtt tta ttc aca ggc aga gaa ttt	736		
Asn Ala Thr Leu Asp Gly Gly Asp Val Leu Phe Thr Gly Arg Glu Phe			
125	130	135	
ttt gtg ggc ctt tcc aaa agg aca aat caa cga ggt gct gaa atc ttg	784		
Phe Val Gly Leu Ser Lys Arg Thr Asn Gln Arg Gly Ala Glu Ile Leu			
140	145	150	
gct gat act ttt aag gac tat gca gtc tcc aca gtg cca gtg gca gat	832		
Ala Asp Thr Phe Lys Asp Tyr Ala Val Ser Thr Val Pro Val Ala Asp			
155	160	165	170
ggg ttg cat ttg aag agt ttc tgc agc atg gct ggg cct aac ctg atc	880		
Gly Leu His Leu Lys Ser Phe Cys Ser Met Ala Gly Pro Asn Leu Ile			
175	180	185	
gca att ggg tct agt gaa tct gca cag aag gcc ctt aag atc atg caa	928		
Ala Ile Gly Ser Ser Glu Ser Ala Gln Lys Ala Leu Lys Ile Met Gln			
190	195	200	
cag atg agt gac cac cgc tac gac aaa ctc act gtg cct gat gac ata	976		
Gln Met Ser Asp His Arg Tyr Asp Lys Leu Thr Val Pro Asp Asp Ile			
205	210	215	
gca gca aac tgt ata tat cta aat atc ccc aac aaa ggg cac gtc ttg	1024		
Ala Ala Asn Cys Ile Tyr Leu Asn Ile Pro Asn Lys Gly His Val Leu			
220	225	230	
ctg cac cga acc ccg gaa gag tat cca gaa agt gca aag gtt tat gag	1072		
Leu His Arg Thr Pro Glu Glu Tyr Pro Glu Ser Ala Lys Val Tyr Glu			
235	240	245	250
aaa ctg aag gac cat atg ctg atc ccc gtg agc atg tct gaa ctg gaa	1120		

Lys Leu Lys Asp His Met Leu Ile Pro Val Ser Met Ser Glu Leu Glu

255 260 265

aag gtg gat ggg ctg ctc acc tgc tgc tca gtt tta att aac aag aaa 1168

Lys Val Asp Gly Leu Leu Thr Cys Cys Ser Val Leu Ile Asn Lys Lys

270 275 280

gta gac tcc tgagctgcag agtccccccc ggtagccggc aagaccgcac 1217

Val Asp Ser

285

aggcaaggcc gatgactctg tgcccactcc tgttgttttc ctgacaatc tactgtgcc 1277

ctgtgctact aactcttggt tacaaaaattt gattctaagt tgaattgctt cattcaacac 1337

ccccaccctc cctccccrcg aggtgggtacc taagctgtgg atttgctaaa tgaattaagc 1397

aacctagaag atacagagct aatgaattat caaaatgiga ttaatcccag taaggaaaca 1457

ctcatttagt gtctgtatct ttgggtgtnaa aattatttag ttgccagtat attctgaaga 1517

atgtcttctt gatcagtcag alaagcttgc tttttttttt tttttttcat gaatcatgtt 1577

tggttcctgt gaaagtcctt ggtccaggga tctctctect ttctctttta ctctctg 1633

<210> 68

<211> 285

<212> PRT

<213> Homo sapiens

<400> 68

Met Ala Gly Leu Gly His Pro Ala Ala Phe Gly Arg Ala Thr His Ala

1 5 10 15

Val Val Arg Ala Leu Pro Glu Ser Leu Gly Gln His Ala Leu Arg Ser

20 25 30

Ala Lys Gly Glu Glu Val Asp Val Ala Arg Ala Glu Arg Gln His Gln

35 40 45

Leu Tyr Val Gly Val Leu Gly Ser Lys Leu Gly Leu Gln Val Val Glu

50

55

60

Leu Pro Ala Asp Glu Ser Leu Pro Asp Cys Val Phe Val Glu Asp Val

65

70

75

80

Ala Val Val Cys Glu Glu Thr Ala Leu Ile Thr Arg Pro Gly Ala Pro

85

90

95

Ser Arg Arg Lys Glu Val Asp Met Met Lys Glu Ala Leu Glu Lys Leu

100

105

110

Gln Leu Asn Ile Val Glu Met Lys Asp Glu Asn Ala Thr Leu Asp Gly

115

120

125

Gly Asp Val Leu Phe Thr Gly Arg Glu Phe Phe Val Gly Leu Ser Lys

130

135

140

Arg Thr Asn Gln Arg Gly Ala Glu Ile Leu Ala Asp Thr Phe Lys Asp

145

150

155

160

Tyr Ala Val Ser Thr Val Pro Val Ala Asp Gly Leu His Leu Lys Ser

165

170

175

Phe Cys Ser Met Ala Gly Pro Asn Leu Ile Ala Ile Gly Ser Ser Glu

180

185

190

Ser Ala Gln Lys Ala Leu Lys Ile Met Gln Gln Met Ser Asp His Arg

195

200

205

Tyr Asp Lys Leu Thr Val Pro Asp Asp Ile Ala Ala Asn Cys Ile Tyr

210

215

220

Leu Asn Ile Pro Asn Lys Gly His Val Leu Leu His Arg Thr Pro Glu

225

230

235

240

Glu Tyr Pro Glu Ser Ala Lys Val Tyr Glu Lys Leu Lys Asp His Met

245

250

255

Leu Ile Pro Val Ser Met Ser Glu Leu Glu Lys Val Asp Gly Leu Leu

260 265 270
 Thr Cys Cys Ser Val Leu Ile Asn Lys Lys Val Asp Ser

275 280 285

<210> 69

<211> 1779

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (147).. (1421)

<400> 69

aagcgctgt ctgaacctct gccagtcctg gagactggig ccctgagctc caaccagcgg 60
 gccatcatc caccctcacc accgcaactt ctaccccgag caagaagcag ctcccagaga 120
 gaaagaacgt tcccacctgc ctagcc atg gga gag gac gct gca cag gcc gaa 173

Met Gly Glu Asp Ala Ala Gln Ala Glu

1 5

aag ttc cag cac cct ggg tct gac atg cgg cag gaa aag ccc tcg agc 221

Lys Phe Gln His Pro Gly Ser Asp Met Arg Gln Glu Lys Pro Ser Ser

10 15 20 25

ccc agc cgg atg cct tcc tcc aca cca agc ccc agc ctg aac cta ggg 269

Pro Ser Pro Met Pro Ser Ser Thr Pro Ser Pro Ser Leu Asn Leu Gly

30 35 40

aac aca gag gag gcc atc cgg gac aac tca cag gtg aac gca gtc acg 317

Asn Thr Glu Glu Ala Ile Arg Asp Asn Ser Gln Val Asn Ala Val Thr

45 50 55

gtg ctc acg ctc ctg gac aag ctg gtg aac atg cta gac gct gtg cag 365

Val	Leu	Thr	Leu	Leu	Asp	Lys	Leu	Val	Asn	Met	Leu	Asp	Ala	Val	Gln		
	60						65					70					
gag aac cag cac aag atg gag cag cga cag atc agt ttg gag ggc tcc																413	
Glu	Asn	Gln	His	Lys	Met	Glu	Gln	Arg	Gln	Ile	Ser	Leu	Glu	Gly	Ser		
	75						80					85					
gtg aag ggc atc cag aat gac ctc acc aag ctc tcc aag tac cag gcc																461	
Val	Lys	Gly	Ile	Gln	Asn	Asp	Leu	Thr	Lys	Leu	Ser	Lys	Tyr	Gln	Ala		
	90					95				100				105			
tcc acc agc aac acg gtg agc aag ctg ctg gag aag tcc cgc aag gtc																509	
Ser	Thr	Ser	Asn	Thr	Val	Ser	Lys	Leu	Leu	Glu	Lys	Ser	Arg	Lys	Val		
					110				115				120				
agc gcc cac acg cgc gcg gtc aaa gag cgc atg gat agg cag tgc gca																557	
Ser	Ala	His	Thr	Arg	Ala	Val	Lys	Glu	Arg	Met	Asp	Arg	Gln	Cys	Ala		
					125				130				135				
cag gtg aag cgg ctg gag aac aac cac gcc cag ctc ctc cga cgc aac																605	
Gln	Val	Lys	Arg	Leu	Glu	Asn	Asn	His	Ala	Gln	Leu	Leu	Arg	Arg	Asn		
					140				145				150				
cat ttc aaa gtg ctc atc ttc cag gag gaa aat gag atc cct gcc agc																653	
His	Phe	Lys	Val	Leu	Ile	Phe	Gln	Glu	Glu	Asn	Glu	Ile	Pro	Ala	Ser		
					155				160				165				
gtg ttt gtg aaa cag ccc gtt tcc ggt gcc gtg gaa ggg aag gag gag																701	
Val	Phe	Val	Lys	Gln	Pro	Val	Ser	Gly	Ala	Val	Glu	Gly	Lys	Glu	Glu		
					170				175				180		185		
ctt ccg gat gaa aac aaa tcc ctg gag gaa acc ctg cac acc gtg gac																749	
Leu	Pro	Asp	Glu	Asn	Lys	Ser	Leu	Glu	Glu	Thr	Leu	His	Thr	Val	Asp		
							190				195				200		

ctc tcc tca gat gat gat ttg ccc cac gat gag gag gcc ctg gaa gac 797
 Leu Ser Ser Asp Asp Asp Leu Pro His Asp Glu Glu Ala Leu Glu Asp
 205 210 215
 agt gcc gag gaa aag gtg gaa gaa agt agg gca gag aaa ata aaa aga 845
 Ser Ala Glu Glu Lys Val Glu Glu Ser Arg Ala Glu Lys Ile Lys Arg
 220 225 230
 tcc agc ctg aag aaa gtg gat agc ctc aag aaa gca ttt tct cgc cag 893
 Ser Ser Leu Lys Lys Val Asp Ser Leu Lys Lys Ala Phe Ser Arg Gln
 235 240 245
 aac atc gag aaa aag atg aac aag ctg ggg aca aag atc gta tct gta 941
 Asn Ile Glu Lys Lys Met Asn Lys Leu Gly Thr Lys Ile Val Ser Val
 250 255 260 265
 gag agg aga gag aag att aag aaa tct ctc acg tca aat cac cag aaa 989
 Glu Arg Arg Glu Lys Ile Lys Lys Ser Leu Thr Ser Asn His Gln Lys
 270 275 280
 ata tcc tca gga aaa agc tcc ccc ttc aag gtt tct ccc ctc act ttc 1037
 Ile Ser Ser Gly Lys Ser Ser Pro Phe Lys Val Ser Pro Leu Thr Phe
 285 290 295
 ggg cgg aag aaa gtc cga gag gga gaa agc cat gca gaa aat gag acc 1085
 Gly Arg Lys Lys Val Arg Glu Gly Glu Ser His Ala Glu Asn Glu Thr
 300 305 310
 aag tca gaa gac ctg cct agc agt gag cag atg cca aat gac cag gaa 1133
 Lys Ser Glu Asp Leu Pro Ser Ser Glu Gln Met Pro Asn Asp Gln Glu
 315 320 325
 gag gag tcc ttt gca gag ggt cat tcc gaa gcg tcc ctc gcc agc gct 1181
 Glu Glu Ser Phe Ala Glu Gly His Ser Glu Ala Ser Leu Ala Ser Ala
 330 335 340 345

ctg gig gaa ggg gaa att gca gag gag gct gct gag aag gcg acc tcc 1229
 Leu Val Glu Gly Glu Ile Ala Glu Glu Ala Ala Glu Lys Ala Thr Ser

350

355

360

agg ggg agt aac tcg ggg atg gac agc aac atc gac ttg act att gtg 1277
 Arg Gly Ser Asn Ser Gly Met Asp Ser Asn Ile Asp Leu Thr Ile Val

365

370

375

gaa gat gaa gag gag gag tca gtg gcc ctg gaa cag gca cag aag gta 1325
 Glu Asp Glu Glu Glu Glu Ser Val Ala Leu Glu Gln Ala Gln Lys Val

380

385

390

cgc tat gag ggt agc tac gcg cta aca tcc gag gag gcg gag cgc tcc 1373
 Arg Tyr Glu Gly Ser Tyr Ala Leu Thr Ser Glu Glu Ala Glu Arg Ser

395

400

405

gat ggg gac ccc gtg cag ccc gcc gtg ctc cag gtg cac cag acc tcc 1421
 Asp Gly Asp Pro Val Gln Pro Ala Val Leu Gln Val His Gln Thr Ser

410

415

420

425

tgagcttaga gccaccgtgc catcctgtgc tgtgctcaag cgggcagcca gggctgaaga 1481
 acaaactcctt gcacatctcc agcacgactc acccactccl gcgttcctgt ccaggcagta 1541
 atcattgacc atatagtcac agtaagacac acgagaccag gctttaccat gaaagcgacc 1601
 tgtcacggac tccactttta atttgcctt aggttctatc tctgtagaat gtctccaaga 1661
 ttgaagaaga aactgagcag ttgaaaaatg ctaatctctt tgacttagtc agaaaaaac 1721
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<210> 70

<211> 425

<212> PRT

<213> Homo sapiens

<400> 70

Met Gly Glu Asp Ala Ala Gln Ala Glu Lys Phe Gln His Pro Gly Ser
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Asp Met Arg Gln Glu Lys Pro Ser Ser Pro Ser Pro Met Pro Ser Ser
20 25 30
Thr Pro Ser Pro Ser Leu Asn Leu Gly Asn Thr Glu Glu Ala Ile Arg
35 40 45
Asp Asn Ser Gln Val Asn Ala Val Thr Val Leu Thr Leu Leu Asp Lys
50 55 60
Leu Val Asn Met Leu Asp Ala Val Gln Glu Asn Gln His Lys Met Glu
65 70 75 80
Gln Arg Gln Ile Ser Leu Glu Gly Ser Val Lys Gly Ile Gln Asn Asp
85 90 95
Leu Thr Lys Leu Ser Lys Tyr Gln Ala Ser Thr Ser Asn Thr Val Ser
100 105 110
Lys Leu Leu Glu Lys Ser Arg Lys Val Ser Ala His Thr Arg Ala Val
115 120 125
Lys Glu Arg Met Asp Arg Gln Cys Ala Gln Val Lys Arg Leu Glu Asn
130 135 140
Asn His Ala Gln Leu Leu Arg Arg Asn His Phe Lys Val Leu Ile Phe
145 150 155 160
Gln Glu Glu Asn Glu Ile Pro Ala Ser Val Phe Val Lys Gln Pro Val
165 170 175
Ser Gly Ala Val Glu Gly Lys Glu Glu Leu Pro Asp Glu Asn Lys Ser
180 185 190
Leu Glu Glu Thr Leu His Thr Val Asp Leu Ser Ser Asp Asp Asp Leu
195 200 205

WO 01/25427

Pro His Asp Glu Glu Ala Leu Glu Asp Ser Ala Glu Glu Lys Val Glu
 210 215 220
 Glu Ser Arg Ala Glu Lys Ile Lys Arg Ser Ser Leu Lys Lys Val Asp
 225 230 235 240
 Ser Leu Lys Lys Ala Phe Ser Arg Gln Asn Ile Glu Lys Lys Met Asn
 245 250 255
 Lys Leu Gly Thr Lys Ile Val Ser Val Glu Arg Arg Glu Lys Ile Lys
 260 265 270
 Lys Ser Leu Thr Ser Asn His Gln Lys Ile Ser Ser Gly Lys Ser Ser
 275 280 285
 Pro Phe Lys Val Ser Pro Leu Thr Phe Gly Arg Lys Lys Val Arg Glu
 290 295 300
 Gly Glu Ser His Ala Glu Asn Glu Thr Lys Ser Glu Asp Leu Pro Ser
 305 310 315 320
 Ser Glu Gln Met Pro Asn Asp Gln Glu Glu Glu Ser Phe Ala Glu Gly
 325 330 335
 His Ser Glu Ala Ser Leu Ala Ser Ala Leu Val Glu Gly Glu Ile Ala
 340 345 350
 Glu Glu Ala Ala Glu Lys Ala Thr Ser Arg Gly Ser Asn Ser Gly Met
 355 360 365
 Asp Ser Asn Ile Asp Leu Thr Ile Val Glu Asp Glu Glu Glu Glu Ser
 370 375 380
 Val Ala Leu Glu Gln Ala Gln Lys Val Arg Tyr Glu Gly Ser Tyr Ala
 385 390 395 400
 Leu Thr Ser Glu Glu Ala Glu Arg Ser Asp Gly Asp Pro Val Gln Pro
 405 410 415
 Ala Val Leu Gln Val His Gln Thr Ser

420

425

<210> 71

<211> 2638

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (288).. (1844)

<400> 71

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 ccagcgtgac cctgacacg tgggtgcagc agcctgcagc tgcctcaagc catggctgaa 180
 cactgactcc cagctgtggg cttcaccatt acagactccc cagggttca aagacttctc 240
 agcttcgagc atggcttttg gctgtcaggg cagctgtaca atagtgga atg ttt gag 296

Met Phe Glu

1

acg gag gca gat gag aag agg gag atg gcc ttg gag gaa ggg aag ggg 344
 Thr Glu Ala Asp Glu Lys Arg Glu Met Ala Leu Glu Glu Gly Lys Gly

5

10

15

cct ggt gcc gag gat tcc cca ccc agc aag gag ccc tct cct ggc cag 392
 Pro Gly Ala Glu Asp Ser Pro Pro Ser Lys Glu Pro Ser Pro Gly Gln

20

25

30

35

gag ctt cct cca gga caa gac ctt cca ccc aac aag gac tcc cct tct 440
 Glu Leu Pro Pro Gly Gln Asp Leu Pro Pro Asn Lys Asp Ser Pro Ser

40

45

50

ggg cag gaa ccc gct ccc agc caa gaa cca ctg tcc agc aaa gac tca 488

Gly Gln Glu Pro Ala Pro Ser Gln Glu Pro Leu Ser Ser Lys Asp Ser
 55 60 65
 gct acc tct gaa gga tcc cct cca ggc cca gat gct ccg ccc agc aag 536
 Ala Thr Ser Glu Gly Ser Pro Pro Gly Pro Asp Ala Pro Pro Ser Lys
 70 75 80
 gat gtc cca cca tgc cag gaa ccc cct cca gcc caa gac ctc tca ccc 584
 Asp Val Pro Pro Cys Gln Glu Pro Pro Pro Ala Gln Asp Leu Ser Pro
 85 90 95
 tgc cag gac cta cct gct ggt caa gaa ccc ctg cct cac cag gac cct 632
 Cys Gln Asp Leu Pro Ala Gly Gln Glu Pro Leu Pro His Gln Asp Pro
 100 105 110 115
 cta ctc acc aaa gac ctc cct gcc atc cag gaa tcc ccc acc cgg gac 680
 Leu Leu Thr Lys Asp Leu Pro Ala Ile Gln Glu Ser Pro Thr Arg Asp
 120 125 130
 ctt cca ccc tgt caa gat ctg cct cct agc cag gtc tcc ctg cca gcc 728
 Leu Pro Pro Cys Gln Asp Leu Pro Pro Ser Gln Val Ser Leu Pro Ala
 135 140 145
 aag gcc ctt act gag gac acc atg agc tcc ggg gac cta cta gca gct 776
 Lys Ala Leu Thr Glu Asp Thr Met Ser Ser Gly Asp Leu Leu Ala Ala
 150 155 160
 act ggg gac cca cct gcg gcc ccc agg cca gcc ttc gtg atc cct gag 824
 Thr Gly Asp Pro Pro Ala Ala Pro Arg Pro Ala Phe Val Ile Pro Glu
 165 170 175
 gtc cgg ctg gat agc acc tac agc cag aag gca ggg gca gag cag ggc 872
 Val Arg Leu Asp Ser Thr Tyr Ser Gln Lys Ala Gly Ala Glu Gln Gly
 180 185 190 195

tgc tgc gga gat gag gag gat gca gaa gag gcc gag gag gtc gag gag	920
Cys Ser Gly Asp Glu Glu Asp Ala Glu Glu Ala Glu Glu Val Glu Glu	
200 205 210	
ggg gag gaa ggg gag gag gac gag gat gag gac acc agc gat gac aac	968
Gly Glu Glu Gly Glu Glu Asp Glu Asp Glu Asp Thr Ser Asp Asp Asn	
215 220 225	
tac gga gag cgc agt gag gcc aag cgc agc agc atg atc gag acg ggc	1016
Tyr Gly Glu Arg Ser Glu Ala Lys Arg Ser Ser Met Ile Glu Thr Gly	
230 235 240	
cag ggg gct gag ggt ggc ctc tca ctg cgt gtc cag aac tcg ctg cgg	1064
Gln Gly Ala Glu Gly Gly Leu Ser Leu Arg Val Gln Asn Ser Leu Arg	
245 250 255	
cgc cgg acg cac agc gag ggc agc ctg ctg cag gag ccc cga ggg ccc	1112
Arg Arg Thr His Ser Glu Gly Ser Leu Leu Gln Glu Pro Arg Gly Pro	
260 265 270 275	
tgc ttt gcc tcc gac acc acc ttg cac tgc tca gac ggt gag ggc gcc	1160
Cys Phe Ala Ser Asp Thr Thr Leu His Cys Ser Asp Gly Glu Gly Ala	
280 285 290	
gcc tcc acc tgg ggc atg cct tcg ccc agc acc ctc aag aaa gag ctg	1208
Ala Ser Thr Trp Gly Met Pro Ser Pro Ser Thr Leu Lys Lys Glu Leu	
295 300 305	
ggc cgc aat ggt ggc tcc atg cac cac ctt tcc ctc ttc ttc aca gga	1256
Gly Arg Asn Gly Gly Ser Met His His Leu Ser Leu Phe Phe Thr Gly	
310 315 320	
cac agg aag atg agc ggg gct gac acc gtt ggg gat gat gac gaa gcc	1304
His Arg Lys Met Ser Gly Ala Asp Thr Val Gly Asp Asp Asp Glu Ala	
325 330 335	


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tcc cgg aag aga aag agc aaa aac cta gcc aag gac atg aag aac aag 1352
Ser Arg Lys Arg Lys Ser Lys Asn Leu Ala Lys Asp Met Lys Asn Lys
340          345          350          355
ctg ggg atc ttc aga cgg cgg aat gag tcc cct gga gcc cct ccc gcg 1400
Leu Gly Ile Phe Arg Arg Arg Asn Glu Ser Pro Gly Ala Pro Pro Ala
          360          365          370
ggc aag gca gac aaa atg atg aag tca ttc aag ccc acc tca gag gaa 1448
Gly Lys Ala Asp Lys Met Met Lys Ser Phe Lys Pro Thr Ser Glu Glu
          375          380          385
gcc ctc aag tgg ggc gag tcc ttg gag aag ctg ctg gtt cac aaa tac 1496
Ala Leu Lys Trp Gly Glu Ser Leu Glu Lys Leu Leu Val His Lys Tyr
          390          395          400
ggg tta gca gtg ttc caa gcc ttc ctt cgc act gag ttc agt gag gag 1544
Gly Leu Ala Val Phe Gln Ala Phe Leu Arg Thr Glu Phe Ser Glu Glu
          405          410          415
aat ctg gag ttc tgg ttg gct tgt gag gac ttc aag aag gtc aag tca 1592
Asn Leu Glu Phe Trp Leu Ala Cys Glu Asp Phe Lys Lys Val Lys Ser
420          425          430          435
cag tcc aag atg gca tcc aag gcc aag aag atc ttt gct gaa tac atc 1640
Gln Ser Lys Met Ala Ser Lys Ala Lys Lys Ile Phe Ala Glu Tyr Ile
          440          445          450
gcg atc cag gca tgc aag gag gtc aac ctg gac tcc tac acg cgg gag 1688
Ala Ile Gln Ala Cys Lys Glu Val Asn Leu Asp Ser Tyr Thr Arg Glu
          455          460          465
cac acc aag gac aac ctg cag agc gtc acg cgg ggc tgc ttc gac ctg 1736
His Thr Lys Asp Asn Leu Gln Ser Val Thr Arg Gly Cys Phe Asp Leu

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470 475 480
 gca cag aag cgc atc ttc ggg ctc atg gaa aag gac tgc tac cct cgc 1784
 Ala Gln Lys Arg Ile Phe Gly Leu Met Glu Lys Asp Ser Tyr Pro Arg
 485 490 495
 ttt ctc cgt tct gac ctc tac ctg gac ctt att aac cag aag aag atg 1832
 Phe Leu Arg Ser Asp Leu Tyr Leu Asp Leu Ile Asn Gln Lys Lys Met
 500 505 510 515
 agt ccc ccg ctt taggggccac tggagtcgag ctacgcgttc acaccaggcg 1884
 Ser Pro Pro Leu
 ggctgggtcc cctgccacc tgcctccctg cccctgtga cggagggggc aagcaagccc 1944
 ccagaggccg tgcctctgga cagacggala gacatacga agcgaggcct ggaccaagag 2004
 agggccaggc tactggagga gtagaaggat gggccccgtg gggccccac tggcccggtg 2064
 cgagggggcc caagacctg gcaggtcagg ggccctggcc aagccagatc tggagctgct 2124
 gctccctgct gcggagaccg cggaggcttc gcgttgacca agttccttaa agaactggct 2184
 gatggggcag gaggtccagg cctgggctct cgggccctcc tagaggggca ttggagcttg 2244
 cagctcagac cccacttgg agttttatit atttaaata tagltggatg cttggcacgt 2304
 cgtcctglaa taggaaaccc ttgcctcacc agttttcctg atttacaagt gcaatatit 2364
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 gggacactgc agtctggcga cacacagaga tctggcacc cctgggtgga gtgtccctcg 2544
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 aaaggccgtg gttatitctt gttcttgaaa aaaa 2638

<210> 72

<211> 519

<212> PRT

<213> Homo sapiens

WO 01/25427

<400> 72

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 Gly Lys Gly Pro Gly Ala Glu Asp Ser Pro Pro Ser Lys Glu Pro Ser
 20 25 30
 Pro Gly Gln Glu Leu Pro Pro Gly Gln Asp Leu Pro Pro Asn Lys Asp
 35 40 45
 Ser Pro Ser Gly Gln Glu Pro Ala Pro Ser Gln Glu Pro Leu Ser Ser
 50 55 60
 Lys Asp Ser Ala Thr Ser Glu Gly Ser Pro Pro Gly Pro Asp Ala Pro
 65 70 75 80
 Pro Ser Lys Asp Val Pro Pro Cys Gln Glu Pro Pro Pro Ala Gln Asp
 85 90 95
 Leu Ser Pro Cys Gln Asp Leu Pro Ala Gly Gln Glu Pro Leu Pro His
 100 105 110
 Gln Asp Pro Leu Leu Thr Lys Asp Leu Pro Ala Ile Gln Glu Ser Pro
 115 120 125
 Thr Arg Asp Leu Pro Pro Cys Gln Asp Leu Pro Pro Ser Gln Val Ser
 130 135 140
 Leu Pro Ala Lys Ala Leu Thr Glu Asp Thr Met Ser Ser Gly Asp Leu
 145 150 155 160
 Leu Ala Ala Thr Gly Asp Pro Pro Ala Ala Pro Arg Pro Ala Phe Val
 165 170 175
 Ile Pro Glu Val Arg Leu Asp Ser Thr Tyr Ser Gln Lys Ala Gly Ala
 180 185 190
 Glu Gln Gly Cys Ser Gly Asp Glu Glu Asp Ala Glu Glu Ala Glu Glu
 195 200 205

WO 01/25427

Val Glu Glu Gly Glu Glu Gly Glu Glu Asp Glu Asp Glu Asp Thr Ser
 210 215 220
 Asp Asp Asn Tyr Gly Glu Arg Ser Glu Ala Lys Arg Ser Ser Met Ile
 225 230 235 240
 Glu Thr Gly Gln Gly Ala Glu Gly Gly Leu Ser Leu Arg Val Gln Asn
 245 250 255
 Ser Leu Arg Arg Arg Thr His Ser Glu Gly Ser Leu Leu Gln Glu Pro
 260 265 270
 Arg Gly Pro Cys Phe Ala Ser Asp Thr Thr Leu His Cys Ser Asp Gly
 275 280 285
 Glu Gly Ala Ala Ser Thr Trp Gly Met Pro Ser Pro Ser Thr Leu Lys
 290 295 300
 Lys Glu Leu Gly Arg Asn Gly Gly Ser Met His His Leu Ser Leu Phe
 305 310 315 320
 Phe Thr Gly His Arg Lys Met Ser Gly Ala Asp Thr Val Gly Asp Asp
 325 330 335
 Asp Glu Ala Ser Arg Lys Arg Lys Ser Lys Asn Leu Ala Lys Asp Met
 340 345 350
 Lys Asn Lys Leu Gly Ile Phe Arg Arg Arg Asn Glu Ser Pro Gly Ala
 355 360 365
 Pro Pro Ala Gly Lys Ala Asp Lys Met Met Lys Ser Phe Lys Pro Thr
 370 375 380
 Ser Glu Glu Ala Leu Lys Trp Gly Glu Ser Leu Glu Lys Leu Leu Val
 385 390 395 400
 His Lys Tyr Gly Leu Ala Val Phe Gln Ala Phe Leu Arg Thr Glu Phe
 405 410 415

Ser Glu Glu Asn Leu Glu Phe Trp Leu Ala Cys Glu Asp Phe Lys Lys

420

425

430

Val Lys Ser Gln Ser Lys Met Ala Ser Lys Ala Lys Lys Ile Phe Ala

435

440

445

Glu Tyr Ile Ala Ile Gln Ala Cys Lys Glu Val Asn Leu Asp Ser Tyr

450

455

460

Thr Arg Glu His Thr Lys Asp Asn Leu Gln Ser Val Thr Arg Gly Cys

465

470

475

480

Phe Asp Leu Ala Gln Lys Arg Ile Phe Gly Leu Met Glu Lys Asp Ser

485

490

495

Tyr Pro Arg Phe Leu Arg Ser Asp Leu Tyr Leu Asp Leu Ile Asn Gln

500

505

510

Lys Lys Met Ser Pro Pro Leu

515

<210> 73

<211> 1901

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (250).. (1206)

<400> 73

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 gtccagggt tggaagatta tctacccgg cccagctat ataagctgac cgggtggag 180
 gggcccagca gggccaactc cagggttcc ttccagaca gaaaaacata caagactcct 240

tcagccaac atg atg gia ctg aaa gia gag gaa ctg gtc act gga aag aag 291

Met Met Val Leu Lys Val Glu Glu Leu Val Thr Gly Lys Lys

1

5

10

aat ggc aat ggg gag gca ggg gaa ttc ctt cct gag gat ttc aga gat 339

Asn Gly Asn Gly Glu Ala Gly Glu Phe Leu Pro Glu Asp Phe Arg Asp

15

20

25

30

gga gag tat gaa gct gct gtt act tta gag aag cag gag gat ctg aag 387

Gly Glu Tyr Glu Ala Ala Val Thr Leu Glu Lys Gln Glu Asp Leu Lys

35

40

45

aca ctt cta gcc cac cct gtg acc ctg ggg gag caa cag tgg aaa agc 435

Thr Leu Leu Ala His Pro Val Thr Leu Gly Glu Gln Gln Trp Lys Ser

50

55

60

gag aaa caa cga gag gca gag ctc cca aag aaa aaa cta gaa caa aga 483

Glu Lys Gln Arg Glu Ala Glu Leu Pro Lys Lys Lys Leu Glu Gln Arg

65

70

75

tcc aag ctt gaa aat tta gaa gac ctt gaa ata atc att caa ctg aag 531

Ser Lys Leu Glu Asn Leu Glu Asp Leu Glu Ile Ile Ile Gln Leu Lys

80

85

90

aaa agg aaa aaa tac agg aaa act aaa gtt cca gtt gta aag gaa cca 579

Lys Arg Lys Lys Tyr Arg Lys Thr Lys Val Pro Val Val Lys Glu Pro

95

100

105

110

gaa cct gaa atc att acg gaa cct gtg gat gtg cct acg ttt ctg aag 627

Glu Pro Glu Ile Ile Thr Glu Pro Val Asp Val Pro Thr Phe Leu Lys

115

120

125

gct gct ctg gag aat aaa ctg cca gta gta gaa aaa ttc ttg tca gac 675

Ala Ala Leu Glu Asn Lys Leu Pro Val Val Glu Lys Phe Leu Ser Asp

130

135

140

aag aac aat cca gat gtt tgt gat gag tat aaa cgg aca gct ctt cat 723
Lys Asn Asn Pro Asp Val Cys Asp Glu Tyr Lys Arg Thr Ala Leu His
145 150 155
aga gca tgc ttg gaa gga cat ttg gca att gtg gag aag tta atg gaa 771
Arg Ala Cys Leu Glu Gly His Leu Ala Ile Val Glu Lys Leu Met Glu
160 165 170
gct gga gcc cag atc gaa ttc cgt gat atg ctt gaa tcc aca gcc atc 819
Ala Gly Ala Gln Ile Glu Phe Arg Asp Met Leu Glu Ser Thr Ala Ile
175 180 185 190
cac tgg gca agc cgt gga gga aac ctg gat gtt tta aaa ttg ttg ctg 867
His Trp Ala Ser Arg Gly Gly Asn Leu Asp Val Leu Lys Leu Leu Leu
195 200 205
aat aaa gga gca aaa att agc gcc cga gat aag ttg ctc agc aca gcg 915
Asn Lys Gly Ala Lys Ile Ser Ala Arg Asp Lys Leu Leu Ser Thr Ala
210 215 220
ctg cat gtg gcg gtg agg act ggc cac tat gag tgc gcg gag cat ctt 963
Leu His Val Ala Val Arg Thr Gly His Tyr Glu Cys Ala Glu His Leu
225 230 235
atc gcc tgt gag gca gac ctc aac gcc aaa gac aga gaa gga gat acc 1011
Ile Ala Cys Glu Ala Asp Leu Asn Ala Lys Asp Arg Glu Gly Asp Thr
240 245 250
ccg ttg cat gat gcg gtg aga ctg aac cgc tat aag atg atc cga ctc 1059
Pro Leu His Asp Ala Val Arg Leu Asn Arg Tyr Lys Met Ile Arg Leu
255 260 265 270
ctg att atg tat ggc gcg gat ctc aac atc aag aac tgt gct ggg aag 1107
Leu Ile Met Tyr Gly Ala Asp Leu Asn Ile Lys Asn Cys Ala Gly Lys

275 280 285
 acg ccg atg gat ctg glg cta cac tgg cag aat gga acc aaa gca ata 1155
 Thr Pro Met Asp Leu Val Leu His Trp Gln Asn Gly Thr Lys Ala Ile
 290 295 300
 ttc gac agc ctc aga gag aac tcc tac aag acc tct cgc ata gct aca 1203
 Phe Asp Ser Leu Arg Glu Asn Ser Tyr Lys Thr Ser Arg Ile Ala Thr
 305 310 315
 ttc tgaggcaaac gacagactct taatcagtaa atgttcactg gcattttgaa 1256
 Phe
 ggcatggccc aggagaagag acactagcca taaaatctag tttctattta tcaacgtgtt 1316
 gigaagatgt acctaaigaa gttttgagaa agcacagggt tataggigt taaatttcct 1376
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 gataatcaga ccttcatgat catccatctg gtgagcagag cttcatttgt atataacact 1496
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 acaggaaagg aaacaalga aggaaagtga ttctgtgaaa aggacagtga agccagctat 1736
 ttaccceca ggctggattt tttttttttt tttttttttt ttttttttta ccgagtacac 1796
 agagiacca agtgaagaga acgicattgag tgtaagtgca aatcagtga aggagcggca 1856
 aactgggaca tgcagaattg aatttgcica aaaaaaaaaa aaaaa 1901

<210> 74

<211> 319

<212> PRT

<213> Homo sapiens

<400> 74

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Tyr Glu Ala Ala Val Thr Leu Glu Lys Gln Glu Asp Leu Lys Thr Leu			
35	40	45	
Leu Ala His Pro Val Thr Leu Gly Glu Gln Gln Trp Lys Ser Glu Lys			
50	55	60	
Gln Arg Glu Ala Glu Leu Pro Lys Lys Lys Leu Glu Gln Arg Ser Lys			
65	70	75	80
Leu Glu Asn Leu Glu Asp Leu Glu Ile Ile Ile Gln Leu Lys Lys Arg			
85	90	95	
Lys Lys Tyr Arg Lys Thr Lys Val Pro Val Val Lys Glu Pro Glu Pro			
100	105	110	
Glu Ile Ile Thr Glu Pro Val Asp Val Pro Thr Phe Leu Lys Ala Ala			
115	120	125	
Leu Glu Asn Lys Leu Pro Val Val Glu Lys Phe Leu Ser Asp Lys Asn			
130	135	140	
Asn Pro Asp Val Cys Asp Glu Tyr Lys Arg Thr Ala Leu His Arg Ala			
145	150	155	160
Cys Leu Glu Gly His Leu Ala Ile Val Glu Lys Leu Met Glu Ala Gly			
165	170	175	
Ala Gln Ile Glu Phe Arg Asp Met Leu Glu Ser Thr Ala Ile His Trp			
180	185	190	
Ala Ser Arg Gly Gly Asn Leu Asp Val Leu Lys Leu Leu Leu Asn Lys			
195	200	205	
Gly Ala Lys Ile Ser Ala Arg Asp Lys Leu Leu Ser Thr Ala Leu His			
210	215	220	

Val Ala Val Arg Thr Gly His Tyr Glu Cys Ala Glu His Leu Ile Ala

225 230 235 240

Cys Glu Ala Asp Leu Asn Ala Lys Asp Arg Glu Gly Asp Thr Pro Leu

245 250 255

His Asp Ala Val Arg Leu Asn Arg Tyr Lys Met Ile Arg Leu Leu Ile

260 265 270

Met Tyr Gly Ala Asp Leu Asn Ile Lys Asn Cys Ala Gly Lys Thr Pro

275 280 285

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290 295 300

Ser Leu Arg Glu Asn Ser Tyr Lys Thr Ser Arg Ile Ala Thr Phe

305 310 315

<210> 75

<211> 5613

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (118).. (5475)

<400> 75

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atg ggg ctt ctc cag ttg cta gct ttc agt ttc tta gcc ctg tgc aga 165

Met Gly Leu Leu Gln Leu Leu Ala Phe Ser Phe Leu Ala Leu Cys Arg

1 5 10 15

gcc cga gtg cgc gct cag gaa ccc gag ttc agc tac ggc tgc gca gaa 213

Ala Arg Val Arg Ala Gln Glu Pro Glu Phe Ser Tyr Gly Cys Ala Glu
 20 25 30
 ggc agc tgc tat ccc gcc acg ggc gac ctt ctc atc ggc cga gca cag 261
 Gly Ser Cys Tyr Pro Ala Thr Gly Asp Leu Leu Ile Gly Arg Ala Gln
 35 40 45
 aag ctt tcg gtg acc tcg acg tgc ggg ctg cac aag ccc gaa ccc tac 309
 Lys Leu Ser Val Thr Ser Thr Cys Gly Leu His Lys Pro Glu Pro Tyr
 50 55 60
 tgt atc gtc agc cac ttg cag gag gac aaa aaa tgc ttc ata tgc aat 357
 Cys Ile Val Ser His Leu Gln Glu Asp Lys Lys Cys Phe Ile Cys Asn
 65 70 75 80
 tcc caa gat cct tat cat gag acc ctg aat cct gac agc cat ctc att 405
 Ser Gln Asp Pro Tyr His Glu Thr Leu Asn Pro Asp Ser His Leu Ile
 85 90 95
 gaa aat gtg gtc act aca ttt gct cca aac cgc ctt aag att tgg tgg 453
 Glu Asn Val Val Thr Thr Phe Ala Pro Asn Arg Leu Lys Ile Trp Trp
 100 105 110
 caa tct gaa aat ggt gtg gaa aat gta act atc caa ctg gat ttg gaa 501
 Gln Ser Glu Asn Gly Val Glu Asn Val Thr Ile Gln Leu Asp Leu Glu
 115 120 125
 gca gaa ttc cat ttt act cat ctc ata atg act ttc aag aca ttc cgt 549
 Ala Glu Phe His Phe Thr His Leu Ile Met Thr Phe Lys Thr Phe Arg
 130 135 140
 cca gct gct atg ctg ata gaa cga tcg tcc gac ttt ggg aaa acc tgg 597
 Pro Ala Ala Met Leu Ile Glu Arg Ser Ser Asp Phe Gly Lys Thr Trp
 145 150 155 160

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ggt gtg tat aga tac ttc gcc tat gac tgt gag gcc tcg ttt cca ggc 645
Gly Val Tyr Arg Tyr Phe Ala Tyr Asp Cys Glu Ala Ser Phe Pro Gly
      165              170              175

att tca act ggc ccc atg aaa aaa gtc gat gac ata att tgt gat tct 693
Ile Ser Thr Gly Pro Met Lys Lys Val Asp Asp Ile Ile Cys Asp Ser
      180              185              190

cga tat tct gac att gaa ccc tca act gaa gga gag gtg ata ttt cgt 741
Arg Tyr Ser Asp Ile Glu Pro Ser Thr Glu Gly Glu Val Ile Phe Arg
      195              200              205

gct tta gat cct gct ttc aaa ata gaa gat cct tat agc cca agg ata 789
Ala Leu Asp Pro Ala Phe Lys Ile Glu Asp Pro Tyr Ser Pro Arg Ile
      210              215              220

cag aat tta tta aaa att acc aac ttg aga atc aag ttt gtg aaa ctg 837
Gln Asn Leu Leu Lys Ile Thr Asn Leu Arg Ile Lys Phe Val Lys Leu
      225              230              235              240

cat act ttg gga gat aac ctt ctg gat tcc agg atg gaa atc aga gaa 885
His Thr Leu Gly Asp Asn Leu Leu Asp Ser Arg Met Glu Ile Arg Glu
      245              250              255

aag tat tat tat gca gtt tat gat atg gtg gtt cga gga aat tgc ttc 933
Lys Tyr Tyr Tyr Ala Val Tyr Asp Met Val Val Arg Gly Asn Cys Phe
      260              265              270

tgc tat ggt cat gcc agc gaa tgt gcc cct glg gat gga ttc aat gaa 981
Cys Tyr Gly His Ala Ser Glu Cys Ala Pro Val Asp Gly Phe Asn Glu
      275              280              285

gaa gtg gaa gga atg gtt cac gga cac tgc atg tgc agg cat aac acc 1029
Glu Val Glu Gly Met Val His Gly His Cys Met Cys Arg His Asn Thr
      290              295              300

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Lys Gly Leu Asn Cys Glu Leu Cys Met Asp Phe Tyr His Asp Leu Pro
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tgg aga cct gct gaa ggc cga aac agc aac gcc tgt aaa aaa tgt aac 1125
Trp Arg Pro Ala Glu Gly Arg Asn Ser Asn Ala Cys Lys Lys Cys Asn
          325          330          335
tgc aat gaa cat tcc atc tct tgt cac ttt gac atg gct gtt tac ctg 1173
Cys Asn Glu His Ser Ile Ser Cys His Phe Asp Met Ala Val Tyr Leu
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gcc acg ggg aac gtc agc gga ggc gtg tgt gat gac tgt cag cac aac 1221
Ala Thr Gly Asn Val Ser Gly Gly Val Cys Asp Asp Cys Gln His Asn
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acc atg ggg cgc aac tgt gag cag tgc aag ccg ttt tac tac cag cac 1269
Thr Met Gly Arg Asn Cys Glu Gln Cys Lys Pro Phe Tyr Tyr Gln His
          370          375          380
cca gag agg gac atc cga gat cct aat ttc tgt gaa cga tgt acg tgt 1317
Pro Glu Arg Asp Ile Arg Asp Pro Asn Phe Cys Glu Arg Cys Thr Cys
385          390          395          400
gac cca gct ggc tct caa aat gag gga att tgt gac agc tat act gat 1365
Asp Pro Ala Gly Ser Gln Asn Glu Gly Ile Cys Asp Ser Tyr Thr Asp
          405          410          415
ttt tct act ggt ctc att gct ggc cag tgt cgg tgt aaa tta aat gtg 1413
Phe Ser Thr Gly Leu Ile Ala Gly Gln Cys Arg Cys Lys Leu Asn Val
          420          425          430
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Glu Gly Glu His Cys Asp Val Cys Lys Glu Gly Phe Tyr Asp Leu Ser

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aca att cct gga ggg aat cct tgt gat tcc gag aca ggt cac tgc tac	1557		
Thr Ile Pro Gly Gly Asn Pro Cys Asp Ser Glu Thr Gly His Cys Tyr			
465	470	475	480
tgc aag cgt ctg gtg aca gga cag cat tgt gac cag tgc ctg cca gag	1605		
Cys Lys Arg Leu Val Thr Gly Gln His Cys Asp Gln Cys Leu Pro Glu			
485	490	495	
cac tgg ggc tta agc aat gat ttg gat gga tgt cga cca tgt gac tgt	1653		
His Trp Gly Leu Ser Asn Asp Leu Asp Gly Cys Arg Pro Cys Asp Cys			
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Asp Leu Gly Gly Ala Leu Asn Asn Ser Cys Phe Ala Glu Ser Gly Gln			
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Pro Gly Tyr Tyr Phe Ala Thr Leu Asp His Tyr Leu Tyr Glu Ala Glu			
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Glu Ala Asn Leu Gly Pro Gly Val Ser Ile Val Glu Arg Gln Tyr Ile			
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Gln Asp Arg Ile Pro Ser Trp Thr Gly Ala Gly Phe Val Arg Val Pro			

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Glu Tyr Asp Ile Leu Ile Arg Tyr Glu Pro Gln Leu Pro Asp His Trp			
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Glu Lys Ala Val Ile Thr Val Gln Arg Pro Gly Arg Ile Pro Thr Ser			
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agc cga tgt ggt aat acc atc ccc gat gat gac aac cag gtg gtg tca			2085
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Leu Ser Pro Gly Ser Arg Tyr Val Val Leu Pro Arg Pro Val Cys Phe			
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Glu Lys Gly Thr Asn Tyr Thr Val Arg Leu Glu Leu Pro Gln Tyr Thr			
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Ser Ser Asp Ser Asp Val Glu Ser Pro Tyr Thr Leu Ile Asp Ser Leu			
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Val Leu Met Pro Tyr Cys Lys Ser Leu Asp Ile Phe Thr Val Gly Gly			
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 Thr Gly Leu Ala Cys Glu Cys Asp Pro Gln Gly Ser Leu Ser Ser Val
 770 775 780
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 Cys Asp Pro Asn Gly Gly Gln Cys Gln Cys Arg Pro Asn Val Val Gly
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Gln Pro Cys Gln Cys Asn Gly His Ala Asp Asp Cys Asp Pro Val Thr
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 Glu Thr Gly Arg Cys Leu Lys Cys Leu Tyr His Thr Glu Gly Glu His
 995 1000 1005

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 1060 1065 1070
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 Trp Gln Leu Ala Ser Gly Thr Gly Cys Asp Pro Cys Asn Cys Asn Ala
 1075 1080 1085
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Leu Glu Ala Glu Glu Arg Val Asn Ala Ser Thr Thr Glu Pro Asn Ser			
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act gtg gag cag tca gcc ctc atg aga gac aga gta gaa gac gtg atg			4197
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<212> PRT

<213> Homo sapiens

<400> 76

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Lys Leu Ser Val Thr Ser Thr Cys Gly Leu His Lys Pro Glu Pro Tyr			
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Cys Ile Val Ser His Leu Gln Glu Asp Lys Lys Cys Phe Ile Cys Asn			
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Ser Gln Asp Pro Tyr His Glu Thr Leu Asn Pro Asp Ser His Leu Ile			
85	90	95	
Glu Asn Val Val Thr Thr Phe Ala Pro Asn Arg Leu Lys Ile Trp Trp			
100	105	110	
Gln Ser Glu Asn Gly Val Glu Asn Val Thr Ile Gln Leu Asp Leu Glu			
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Ala Glu Phe His Phe Thr His Leu Ile Met Thr Phe Lys Thr Phe Arg			
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Pro Ala Ala Met Leu Ile Glu Arg Ser Ser Asp Phe Gly Lys Thr Trp			
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Arg Tyr Ser Asp Ile Glu Pro Ser Thr Glu Gly Glu Val Ile Phe Arg			
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Ala Leu Asp Pro Ala Phe Lys Ile Glu Asp Pro Tyr Ser Pro Arg Ile			
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His Thr Leu Gly Asp Asn Leu Leu Asp Ser Arg Met Glu Ile Arg Glu			

245 250 255
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260 265 270
Cys Tyr Gly His Ala Ser Glu Cys Ala Pro Val Asp Gly Phe Asn Glu
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Lys Gly Leu Asn Cys Glu Leu Cys Met Asp Phe Tyr His Asp Leu Pro
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325 330 335
Cys Asn Glu His Ser Ile Ser Cys His Phe Asp Met Ala Val Tyr Leu
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Thr Ile Pro Gly Gly Asn Pro Cys Asp Ser Glu Thr Gly His Cys Tyr
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 His Trp Gly Leu Ser Asn Asp Leu Asp Gly Cys Arg Pro Cys Asp Cys
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 625 630 635 640
 Ser Arg Cys Gly Asn Thr Ile Pro Asp Asp Asp Asn Gln Val Val Ser
 645 650 655
 Leu Ser Pro Gly Ser Arg Tyr Val Val Leu Pro Arg Pro Val Cys Phe
 660 665 670

Glu Lys Gly Thr Asn Tyr Thr Val Arg Leu Glu Leu Pro Gln Tyr Thr
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785 790 795 800
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820 825 830
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835 840 845
Arg Gln Cys Asp Arg Cys Leu Pro Gly His Trp Gly Phe Pro Ser Cys
850 855 860
Gln Pro Cys Gln Cys Asn Gly His Ala Asp Asp Cys Asp Pro Val Thr
865 870 875 880
Gly Glu Cys Leu Asn Cys Gln Asp Tyr Thr Met Gly His Asn Cys Glu

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	885	890	895
Arg Cys Leu Ala Gly Tyr Tyr Gly Asp Pro Ile Ile Gly Ser Gly Asp			
	900	905	910
His Cys Arg Pro Cys Pro Cys Pro Asp Gly Pro Asp Ser Gly Arg Gln			
	915	920	925
Phe Ala Arg Ser Cys Tyr Gln Asp Pro Val Thr Leu Gln Leu Ala Cys			
	930	935	940
Val Cys Asp Pro Gly Tyr Ile Gly Ser Arg Cys Asp Asp Cys Ala Ser			
	945	950	955
Gly Tyr Phe Gly Asn Pro Ser Glu Val Gly Gly Ser Cys Gln Pro Cys			960
	965	970	975
Gln Cys His Asn Asn Ile Asp Thr Thr Asp Pro Glu Ala Cys Asp Lys			
	980	985	990
Glu Thr Gly Arg Cys Leu Lys Cys Leu Tyr His Thr Glu Gly Glu His			
	995	1000	1005
Cys Gln Phe Cys Arg Phe Gly Tyr Tyr Gly Asp Ala Leu Arg Gln Asp			
	1010	1015	1020
Cys Arg Lys Cys Val Cys Asn Tyr Leu Gly Thr Val Gln Glu His Cys			
	1025	1030	1035
Asn Gly Ser Asp Cys Gln Cys Asp Lys Ala Thr Gly Gln Cys Leu Cys			1040
	1045	1050	1055
Leu Pro Asn Val Ile Gly Gln Asn Cys Asp Arg Cys Ala Pro Asn Thr			
	1060	1065	1070
Trp Gln Leu Ala Ser Gly Thr Gly Cys Asp Pro Cys Asn Cys Asn Ala			
	1075	1080	1085
Ala His Ser Phe Gly Pro Ser Cys Asn Glu Phe Thr Gly Gln Cys Gln			

1090	1095	1100	
Cys Met Pro Gly Phe Gly Gly Arg Thr Cys Ser Glu Cys Gln Glu Leu			
1105	1110	1115	1120
Phe Trp Gly Asp Pro Asp Val Glu Cys Arg Ala Cys Asp Cys Asp Pro			
1125	1130	1135	
Arg Gly Ile Glu Thr Pro Gln Cys Asp Gln Ser Thr Gly Gln Cys Val			
1140	1145	1150	
Cys Val Glu Gly Val Glu Gly Pro Arg Cys Asp Lys Cys Thr Arg Gly			
1155	1160	1165	
Tyr Ser Gly Val Phe Pro Asp Cys Thr Pro Cys His Gln Cys Phe Ala			
1170	1175	1180	
Leu Trp Asp Val Ile Ile Ala Glu Leu Thr Asn Arg Thr His Arg Phe			
1185	1190	1195	1200
Leu Glu Lys Ala Lys Ala Leu Lys Ile Ser Gly Val Ile Gly Pro Tyr			
1205	1210	1215	
Arg Glu Thr Val Asp Ser Val Glu Arg Lys Val Ser Glu Ile Lys Asp			
1220	1225	1230	
Ile Leu Ala Gln Ser Pro Ala Ala Glu Pro Leu Lys Asn Ile Gly Asn			
1235	1240	1245	
Leu Phe Glu Glu Ala Glu Lys Leu Ile Lys Asp Val Thr Glu Met Met			
1250	1255	1260	
Ala Gln Val Glu Val Lys Leu Ser Asp Thr Thr Ser Gln Ser Asn Ser			
1265	1270	1275	1280
Thr Ala Lys Glu Leu Asp Ser Leu Gln Thr Glu Ala Glu Ser Leu Asp			
1285	1290	1295	
Asn Thr Val Lys Glu Leu Ala Glu Gln Leu Glu Phe Ile Lys Asn Ser			
1300	1305	1310	

Asp Ile Arg Gly Ala Leu Asp Ser Ile Thr Lys Tyr Phe Gln Met Ser
 1315 1320 1325
 Leu Glu Ala Glu Glu Arg Val Asn Ala Ser Thr Thr Glu Pro Asn Ser
 1330 1335 1340
 Thr Val Glu Gln Ser Ala Leu Met Arg Asp Arg Val Glu Asp Val Met
 1345 1350 1355 1360
 Met Glu Arg Glu Ser Gln Phe Lys Glu Lys Gln Glu Glu Gln Ala Arg
 1365 1370 1375
 Leu Leu Asp Glu Leu Ala Gly Lys Leu Gln Ser Leu Asp Leu Ser Ala
 1380 1385 1390
 Ala Ala Glu Met Thr Cys Gly Thr Pro Pro Gly Ala Ser Cys Ser Glu
 1395 1400 1405
 Thr Glu Cys Gly Gly Pro Asn Cys Arg Thr Asp Glu Gly Glu Arg Lys
 1410 1415 1420
 Cys Gly Gly Pro Gly Cys Gly Gly Leu Val Thr Val Ala His Asn Ala
 1425 1430 1435 1440
 Trp Gln Lys Ala Met Asp Leu Asp Gln Asp Val Leu Ser Ala Leu Ala
 1445 1450 1455
 Glu Val Glu Gln Leu Ser Lys Met Val Ser Glu Ala Lys Leu Arg Ala
 1460 1465 1470
 Asp Glu Ala Lys Gln Ser Ala Glu Asp Ile Leu Leu Lys Thr Asn Ala
 1475 1480 1485
 Thr Lys Glu Lys Met Asp Lys Ser Asn Glu Glu Leu Arg Asn Leu Ile
 1490 1495 1500
 Lys Gln Ile Arg Asn Phe Leu Thr Gln Asp Ser Ala Asp Leu Asp Ser
 1505 1510 1515 1520

Ile Glu Ala Val Ala Asn Glu Val Leu Lys Met Glu Met Pro Ser Thr
1525 1530 1535
Pro Gln Gln Leu Gln Asn Leu Thr Glu Asp Ile Arg Glu Arg Val Glu
1540 1545 1550
Ser Leu Ser Gln Val Glu Val Ile Leu Gln His Ser Ala Ala Asp Ile
1555 1560 1565
Ala Arg Ala Glu Met Leu Leu Glu Glu Ala Lys Arg Ala Ser Lys Ser
1570 1575 1580
Ala Thr Asp Val Lys Val Thr Ala Asp Met Val Lys Glu Ala Leu Glu
1585 1590 1595 1600
Glu Ala Glu Lys Ala Gln Val Ala Ala Glu Lys Ala Ile Lys Gln Ala
1605 1610 1615
Asp Glu Asp Ile Gln Gly Thr Gln Asn Leu Leu Thr Ser Ile Glu Ser
1620 1625 1630
Glu Thr Ala Ala Ser Glu Glu Thr Leu Phe Asn Ala Ser Gln Arg Ile
1635 1640 1645
Ser Glu Leu Glu Arg Asn Val Glu Glu Leu Lys Arg Lys Ala Ala Gln
1650 1655 1660
Asn Ser Gly Glu Ala Glu Tyr Ile Glu Lys Val Val Tyr Thr Val Lys
1665 1670 1675 1680
Gln Ser Ala Glu Asp Val Lys Lys Thr Leu Asp Gly Glu Leu Asp Glu
1685 1690 1695
Lys Tyr Lys Lys Val Glu Asn Leu Ile Ala Lys Lys Thr Glu Glu Ser
1700 1705 1710
Ala Asp Ala Arg Arg Lys Ala Glu Met Leu Gln Asn Glu Ala Lys Thr
1715 1720 1725
Leu Leu Ala Gln Ala Asn Ser Lys Leu Gln Leu Leu Lys Asp Leu Glu

1730	1735	1740	
Arg Lys Tyr Glu Asp Asn Gln Arg Tyr Leu Glu Asp Lys Ala Gln Glu			
1745	1750	1755	1760
Leu Ala Arg Leu Glu Gly Glu Val Arg Ser Leu Leu Lys Asp Ile Ser			
	1765	1770	1775
Gln Lys Val Ala Val Tyr Ser Thr Cys Leu			
1780	1785		

<210> 77

<211> 585

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (27) .. (335)

<400> 77

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Met Lys Ser Leu Ile Leu Leu Ala Ile

1 5

ctg gcc gcc tta gcg gta gta act ttg tgt tat gaa tca cat gaa agc 101

Leu Ala Ala Leu Ala Val Val Thr Leu Cys Tyr Glu Ser His Glu Ser

10 15 20 25

atg gaa tct tat gaa ctt aat ccc ttc att aac agg aga aat gca aat 149

Met Glu Ser Tyr Glu Leu Asn Pro Phe Ile Asn Arg Arg Asn Ala Asn

30 35 40

acc ttc ata tcc cct cag cag aga tgg aga gct aaa gtc caa gag agg 197

Thr Phe Ile Ser Pro Gln Gln Arg Trp Arg Ala Lys Val Gln Glu Arg

45 50 55
 atc cga gaa cgc tct aag cct gtc cac gag ctc aat agg gaa gcc tgt 245
 Ile Arg Glu Arg Ser Lys Pro Val His Glu Leu Asn Arg Glu Ala Cys
 60 65 70
 gat gac tac aga ctt tgc gaa cgc tac gcc atg gtt tat gga tac aat 293
 Asp Asp Tyr Arg Leu Cys Glu Arg Tyr Ala Met Val Tyr Gly Tyr Asn
 75 80 85
 gct gcc tat aat cgc tac ttc agg aag cgc cga ggg acc aaa 335
 Ala Ala Tyr Asn Arg Tyr Phe Arg Lys Arg Arg Gly Thr Lys
 90 95 100
 tgagactgag ggaagaaaaa aaatctcttt tticttggag gctggcacct gattttgtat 395
 cccctgttag cagcattact gaaatacata ggcttatata caatgcctct ttcctgtata 455
 ttctcttgtc tggctgcacc cctttttccc gccccagat tgataagtaa tgaaagtgca 515
 ctgcagtgag ggtcaaagga gagtcaacat aigtgattgt tccataataa acttctgggtg 575
 tgatactttc 585

<210> 78

<211> 103

<212> PRT

<213> Homo sapiens

<400> 78

Met Lys Ser Leu Ile Leu Leu Ala Ile Leu Ala Ala Leu Ala Val Val

1

5

10

15

Thr Leu Cys Tyr Glu Ser His Glu Ser Met Glu Ser Tyr Glu Leu Asn

20

25

30

Pro Phe Ile Asn Arg Arg Asn Ala Asn Thr Phe Ile Ser Pro Gln Gln

35

40

45

Arg Trp Arg Ala Lys Val Gln Glu Arg Ile Arg Glu Arg Ser Lys Pro

50

55

60

Val His Glu Leu Asn Arg Glu Ala Cys Asp Asp Tyr Arg Leu Cys Glu

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80

Arg Tyr Ala Met Val Tyr Gly Tyr Asn Ala Ala Tyr Asn Arg Tyr Phe

85

90

95

Arg Lys Arg Arg Gly Thr Lys

100

<210> 79

<211> 1775

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (6).. (1148)

<400> 79

cagca atg cat ctc ctt gcg att ctg ttt tgt gct ctc tgg tct gca gtg 50

Met His Leu Leu Ala Ile Leu Phe Cys Ala Leu Trp Ser Ala Val

1

5

10

15

ttg gcc gag aac tcg gat gat tat gat ctc atg tat gtg aat ttg gac 98

Leu Ala Glu Asn Ser Asp Asp Tyr Asp Leu Met Tyr Val Asn Leu Asp

20

25

30

aac gaa ala gac aat gga ctc cat ccc act gag gac ccc acg ccg tgc 146

Asn Glu Ile Asp Asn Gly Leu His Pro Thr Glu Asp Pro Thr Pro Cys

35

40

45

gcc tgc ggt cag gag cac tcg gaa tgg gac aag ctc ttc atc atg ctg 194

Ala Cys Gly Gln Glu His Ser Glu Trp Asp Lys Leu Phe Ile Met Leu
 50 55 60
 gag aac tcg cag atg aga gag cgc atg ctg ctg caa gcc acg gac gac 242
 Glu Asn Ser Gln Met Arg Glu Arg Met Leu Leu Gln Ala Thr Asp Asp
 65 70 75
 gtc ctg cgg ggc gag ctg cag agg ctg cgg gag gag ctg ggc cgg ctc 290
 Val Leu Arg Gly Glu Leu Gln Arg Leu Arg Glu Glu Leu Gly Arg Leu
 80 85 90 95
 gcg gaa agc ctg gcg agg ccg tgc gcg ccg ggg gct ccc gca gag gcc 338
 Ala Glu Ser Leu Ala Arg Pro Cys Ala Pro Gly Ala Pro Ala Glu Ala
 100 105 110
 agg ctg acc agt gct ctg gac gag ctg ctg cag gcg acc cgc gac gcg 386
 Arg Leu Thr Ser Ala Leu Asp Glu Leu Leu Gln Ala Thr Arg Asp Ala
 115 120 125
 ggc cgc agg ctg gcg cgt atg gag ggc gcg gag gcg cag cgc cca gag 434
 Gly Arg Arg Leu Ala Arg Met Glu Gly Ala Glu Ala Gln Arg Pro Glu
 130 135 140
 gag gcg ggg cgc gcc ctg gcc gcg gtg cta gag gag ctg cgg cag acg 482
 Glu Ala Gly Arg Ala Leu Ala Ala Val Leu Glu Glu Leu Arg Gln Thr
 145 150 155
 cga gcc gac ctg cac gcg gtg cag ggc tgg gct gcc cgg agc tgg ctg 530
 Arg Ala Asp Leu His Ala Val Gln Gly Trp Ala Ala Arg Ser Trp Leu
 160 165 170 175
 ccg gca ggt tgt gaa aca gct att tta ttc cca atg cgt tcc aag aag 578
 Pro Ala Gly Cys Glu Thr Ala Ile Leu Phe Pro Met Arg Ser Lys Lys
 180 185 190

att ttt gga agc gtg cat cca gtg aga cca atg agg ctt gag tct ttt 626
 Ile Phe Gly Ser Val His Pro Val Arg Pro Met Arg Leu Glu Ser Phe
 195 200 205
 agt gcc tgc att tgg gtc aaa gcc aca gat gta tta aac aaa acc atc 674
 Ser Ala Cys Ile Trp Val Lys Ala Thr Asp Val Leu Asn Lys Thr Ile
 210 215 220
 ctg ttt tcc tat ggc aca aag agg aat cca tat gaa atc cag ctg tat 722
 Leu Phe Ser Tyr Gly Thr Lys Arg Asn Pro Tyr Glu Ile Gln Leu Tyr
 225 230 235
 ctc agc tac caa tcc ata gtg ttt gtg gtg ggt gga gag gag aac aaa 770
 Leu Ser Tyr Gln Ser Ile Val Phe Val Val Gly Gly Glu Glu Asn Lys
 240 245 250 255
 ctg gtt gct gaa gcc atg gtt tcc ctg gga agg tgg acc cac ctg tgc 818
 Leu Val Ala Glu Ala Met Val Ser Leu Gly Arg Trp Thr His Leu Cys
 260 265 270
 ggc acc tgg aat tca gag gaa ggg ctc aca tcc ttg tgg gta aat ggt 866
 Gly Thr Trp Asn Ser Glu Glu Gly Leu Thr Ser Leu Trp Val Asn Gly
 275 280 285
 gaa ctg gcg gct acc act gtt gag atg gcc aca ggt cac att gtt cct 914
 Glu Leu Ala Ala Thr Thr Val Glu Met Ala Thr Gly His Ile Val Pro
 290 295 300
 gag gga gga atc ctg cag att ggc caa gaa aag aat ggc tgc tgt gtg 962
 Glu Gly Gly Ile Leu Gln Ile Gly Gln Glu Lys Asn Gly Cys Cys Val
 305 310 315
 ggt ggt ggc ttt gat gaa aca tta gcc ttc tct ggg aga ctc aca ggc 1010
 Gly Gly Gly Phe Asp Glu Thr Leu Ala Phe Ser Gly Arg Leu Thr Gly
 320 325 330 335

ttc aat atc tgg gat agt gtt ctt agc aat gaa gag ata aga gag acc 1058

Phe Asn Ile Trp Asp Ser Val Leu Ser Asn Glu Glu Ile Arg Glu Thr

340

345

350

gga gga gca gag tct tgt cac atc cgg ggg aat att gtt ggg tgg gga 1106

Gly Gly Ala Glu Ser Cys His Ile Arg Gly Asn Ile Val Gly Trp Gly

355

360

365

gtc aca gag atc cag cca cat gga gga gct cag tat gtt tca 1148

Val Thr Glu Ile Gln Pro His Gly Gly Ala Gln Tyr Val Ser

370

375

380

taaattgttgt gaaactccac ttgaagccaa agaaagaaac tcacacttaa aacacatgcc 1208

agttggaag gtctgaaaac tcagtgcata ataggaacac ttgagactaa tgaaagagag 1268

agttgagacc aatctttatt tglactggcc aaatactgaa taaacagttg aaggaaagac 1328

attggaaaaa gcttttgagg ataattgttac tagactttat gccatgggtgc tttcagttta 1388

atgctgtgtc tctgtcagat aaactctcaa ataattaaaa aggactgtat tgttgaacag 1448

agggacaatt gttttacttt tctttgggta attttgtttt ggccagagat gaattttaca 1508

ttggaagaat aacaaaataa gatttgttgt ccattgttca ttgttatagg tatgtacctt 1568

attacaaaaa aaatgatgaa aacatattta tactacaagg tgacttaaca actataaatg 1628

tagtttaigt gttataatcg aatgtcacgt ttttgagaag atagtcatat aagttatatt 1688

gcaaaaggga tttgtattaa ttttaagacta tttttgtaaa gctctactgt aaataaaaata 1748

ttttataaaa ctaaaaaaaa aaaaaaa 1775

<210> 80

<211> 381

<212> PRT

<213> Homo sapiens

<400> 80

Met His Leu Leu Ala Ile Leu Phe Cys Ala Leu Trp Ser Ala Val Leu

1	5	10	15
Ala Glu Asn Ser Asp Asp Tyr Asp Leu Met Tyr Val Asn Leu Asp Asn			
20	25	30	
Glu Ile Asp Asn Gly Leu His Pro Thr Glu Asp Pro Thr Pro Cys Ala			
35	40	45	
Cys Gly Gln Glu His Ser Glu Trp Asp Lys Leu Phe Ile Met Leu Glu			
50	55	60	
Asn Ser Gln Met Arg Glu Arg Met Leu Leu Gln Ala Thr Asp Asp Val			
65	70	75	80
Leu Arg Gly Glu Leu Gln Arg Leu Arg Glu Glu Leu Gly Arg Leu Ala			
85	90	95	
Glu Ser Leu Ala Arg Pro Cys Ala Pro Gly Ala Pro Ala Glu Ala Arg			
100	105	110	
Leu Thr Ser Ala Leu Asp Glu Leu Leu Gln Ala Thr Arg Asp Ala Gly			
115	120	125	
Arg Arg Leu Ala Arg Met Glu Gly Ala Glu Ala Gln Arg Pro Glu Glu			
130	135	140	
Ala Gly Arg Ala Leu Ala Ala Val Leu Glu Glu Leu Arg Gln Thr Arg			
145	150	155	160
Ala Asp Leu His Ala Val Gln Gly Trp Ala Ala Arg Ser Trp Leu Pro			
165	170	175	
Ala Gly Cys Glu Thr Ala Ile Leu Phe Pro Met Arg Ser Lys Lys Ile			
180	185	190	
Phe Gly Ser Val His Pro Val Arg Pro Met Arg Leu Glu Ser Phe Ser			
195	200	205	
Ala Cys Ile Trp Val Lys Ala Thr Asp Val Leu Asn Lys Thr Ile Leu			

210 215 220
Phe Ser Tyr Gly Thr Lys Arg Asn Pro Tyr Glu Ile Gln Leu Tyr Leu
225 230 235 240
Ser Tyr Gln Ser Ile Val Phe Val Val Gly Gly Glu Glu Asn Lys Leu
245 250 255
Val Ala Glu Ala Met Val Ser Leu Gly Arg Trp Thr His Leu Cys Gly
260 265 270
Thr Trp Asn Ser Glu Glu Gly Leu Thr Ser Leu Trp Val Asn Gly Glu
275 280 285
Leu Ala Ala Thr Thr Val Glu Met Ala Thr Gly His Ile Val Pro Glu
290 295 300
Gly Gly Ile Leu Gln Ile Gly Gln Glu Lys Asn Gly Cys Cys Val Gly
305 310 315 320
Gly Gly Phe Asp Glu Thr Leu Ala Phe Ser Gly Arg Leu Thr Gly Phe
325 330 335
Asn Ile Trp Asp Ser Val Leu Ser Asn Glu Glu Ile Arg Glu Thr Gly
340 345 350
Gly Ala Glu Ser Cys His Ile Arg Gly Asn Ile Val Gly Trp Gly Val
355 360 365
Thr Glu Ile Gln Pro His Gly Gly Ala Gln Tyr Val Ser
370 375 380

<210> 81

<211> 2312

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (146).. (1192)

<400> 81

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 ccaccitccga ccaccgccag cgctccaggc cccgcgcctc ccgcctcgccg ccaccgcgcc 120
 ctccgctccg cccgcagtgc caacc atg acc gcc gcc agt atg ggc ccc gtc 172

Met Thr Ala Ala Ser Met Gly Pro Val

1

5

cgc gtc gcc ttc gtg gtc ctc ctc gcc ctc tgc agc cgg ccg gcc gtc 220

Arg Val Ala Phe Val Val Leu Leu Ala Leu Cys Ser Arg Pro Ala Val

10

15

20

25

ggc cag aac tgc agc ggg ccg tgc cgg tgc ccg gac gag ccg gcg ccg 268

Gly Gln Asn Cys Ser Gly Pro Cys Arg Cys Pro Asp Glu Pro Ala Pro

30

35

40

cgc tgc ccg gcg ggc gtg agc ctc gtg ctg gac ggc tgc ggc tgc tgc 316

Arg Cys Pro Ala Gly Val Ser Leu Val Leu Asp Gly Cys Gly Cys Cys

45

50

55

cgc gtc tgc gcc aag cag ctg ggc gag ctg tgc acc gag cgc gac ccc 364

Arg Val Cys Ala Lys Gln Leu Gly Glu Leu Cys Thr Glu Arg Asp Pro

60

65

70

tgc gac ccg cac aag ggc ctc ttc tgt gac ttc ggc tcc ccg gcc aac 412

Cys Asp Pro His Lys Gly Leu Phe Cys Asp Phe Gly Ser Pro Ala Asn

75

80

85

cgc aag atc ggc gtg tgc acc gcc aaa gat ggt gct ccc tgc atc ttc 460

Arg Lys Ile Gly Val Cys Thr Ala Lys Asp Gly Ala Pro Cys Ile Phe

90

95

100

105

ggt ggt acg gtg tac cgc agc gga gag tcc ttc cag agc agc tgc aag 508

Gly Gly Thr Val Tyr Arg Ser Gly Glu Ser Phe Gln Ser Ser Cys Lys
 110 115 120
 tac cag tgc acg tgc ctg gac ggg gcg glg ggc tgc atg ccc ctg tgc 556
 Tyr Gln Cys Thr Cys Leu Asp Gly Ala Val Gly Cys Met Pro Leu Cys
 125 130 135
 agc atg gac gtt cgt ctg ccc agc cct gac tgc ccc ttc ccg agg agg 604
 Ser Met Asp Val Arg Leu Pro Ser Pro Asp Cys Pro Phe Pro Arg Arg
 140 145 150
 gtc aag ctg ccc ggg aaa tgc tgc gag gag tgg gtg tgt gac gag ccc 652
 Val Lys Leu Pro Gly Lys Cys Cys Glu Glu Trp Val Cys Asp Glu Pro
 155 160 165
 aag gac caa acc gtg gtt ggg cct gcc ctg gcg gct tac cga ctg gaa 700
 Lys Asp Gln Thr Val Val Gly Pro Ala Leu Ala Ala Tyr Arg Leu Glu
 170 175 180 185
 gac acg ttt ggc cca gac cca act atg att aga gcc aac tgc ctg gtc 748
 Asp Thr Phe Gly Pro Asp Pro Thr Met Ile Arg Ala Asn Cys Leu Val
 190 195 200
 cag acc aca gag tgg agc gcc tgt tcc aag acc tgt ggg atg ggc atc 796
 Gln Thr Thr Glu Trp Ser Ala Cys Ser Lys Thr Cys Gly Met Gly Ile
 205 210 215
 tcc acc cgg gtt acc aat gac aac gcc tcc tgc agg cta gag aag cag 844
 Ser Thr Arg Val Thr Asn Asp Asn Ala Ser Cys Arg Leu Glu Lys Gln
 220 225 230
 agc cgc ctg tgc atg gtc agg cct tgc gaa gct gac ctg gaa gag aac 892
 Ser Arg Leu Cys Met Val Arg Pro Cys Glu Ala Asp Leu Glu Glu Asn
 235 240 245

att aag aag ggc aaa aag tgc atc cgt act ccc aaa atc tcc aag cct 940
 Ile Lys Lys Gly Lys Lys Cys Ile Arg Thr Pro Lys Ile Ser Lys Pro
 250 255 260 265
 atc aag ttt gag ctt tct ggc tgc acc agc atg aag aca tac cga gct 988
 Ile Lys Phe Glu Leu Ser Gly Cys Thr Ser Met Lys Thr Tyr Arg Ala
 270 275 280
 aaa ttc tgt gga gla tgt acc gac ggc cga tgc tgc acc ccc cac aga 1036
 Lys Phe Cys Gly Val Cys Thr Asp Gly Arg Cys Cys Thr Pro His Arg
 285 290 295
 acc acc acc ctg ccg gtg gag ttc aag tgc cct gac ggc gag gtc atg 1084
 Thr Thr Thr Leu Pro Val Glu Phe Lys Cys Pro Asp Gly Glu Val Met
 300 305 310
 aag aag aac atg atg ttc atc aag acc tgt gcc tgc cat tac aac tgt 1132
 Lys Lys Asn Met Met Phe Ile Lys Thr Cys Ala Cys His Tyr Asn Cys
 315 320 325
 ccc gga gac aat gac atc ttt gaa tcg ctg tac tac agg aag atg tac 1180
 Pro Gly Asp Asn Asp Ile Phe Glu Ser Leu Tyr Tyr Arg Lys Met Tyr
 330 335 340 345
 gga gac atg gca tgaagccaga gaggtagaga cattaactca ttagactgga 1232
 Gly Asp Met Ala
 acttgaacig attcacatct cttttttccg taaaaatgat ttcagtagca caagtatttt 1292
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 aactacatta gtacacagca ccagaatgta tattaaggig tggctttagg agcagtggga 1472
 gggtaccagc agaaaggta gtatcatcag atagctctta tacgaglaa atgcttgcta 1532
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cagaacagca gactcagctc tgacattctg attcgaatga cactgttcag gaatcggaat 1712
 ccigtcgatt agactggaca gcttctggca agigaatttc ctgtaacaag ccagattttt 1772
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 gatatttcaa tgitagccctc aatttctgaa caccaatagg agaatgtaaa gcttgtctga 1952
 tcgttcaaag catgaaatgg atacttataat ggaaattctc tcagatagaa tgacagtccg 2012
 tcaaaacaga ttgtttgcaa aggggaggca tcagtgtcct tggcaggctg atttctaggt 2072
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 tgactctata tagctgatca gttttttcac ctggaagcat ttgtttctac tttgatatga 2192
 ctgtttttcg gacagttaat ttgttgagag tgtgacaaaa agttacaatgt ttgcaccttt 2252
 ctagttgaaa ataaagtata ttttttctaa aaaaaaaaaa aaacgacagc aacggaattc 2312

<210> 82

<211> 349

<212> PRT

<213> Homo sapiens

<400> 82

Met Thr Ala Ala Ser Met Gly Pro Val Arg Val Ala Phe Val Val Leu

1 5 10 15

Leu Ala Leu Cys Ser Arg Pro Ala Val Gly Gln Asn Cys Ser Gly Pro

20 25 30

Cys Arg Cys Pro Asp Glu Pro Ala Pro Arg Cys Pro Ala Gly Val Ser

35 40 45

Leu Val Leu Asp Gly Cys Gly Cys Cys Arg Val Cys Ala Lys Gln Leu

50 55 60

Gly Glu Leu Cys Thr Glu Arg Asp Pro Cys Asp Pro His Lys Gly Leu

65 70 75 80

Phe Cys Asp Phe Gly Ser Pro Ala Asn Arg Lys Ile Gly Val Cys Thr			
	85	90	95
Ala Lys Asp Gly Ala Pro Cys Ile Phe Gly Gly Thr Val Tyr Arg Ser			
	100	105	110
Gly Glu Ser Phe Gln Ser Ser Cys Lys Tyr Gln Cys Thr Cys Leu Asp			
	115	120	125
Gly Ala Val Gly Cys Met Pro Leu Cys Ser Met Asp Val Arg Leu Pro			
	130	135	140
Ser Pro Asp Cys Pro Phe Pro Arg Arg Val Lys Leu Pro Gly Lys Cys			
	145	150	155
Cys Glu Glu Trp Val Cys Asp Glu Pro Lys Asp Gln Thr Val Val Gly			
	165	170	175
Pro Ala Leu Ala Ala Tyr Arg Leu Glu Asp Thr Phe Gly Pro Asp Pro			
	180	185	190
Thr Met Ile Arg Ala Asn Cys Leu Val Gln Thr Thr Glu Trp Ser Ala			
	195	200	205
Cys Ser Lys Thr Cys Gly Met Gly Ile Ser Thr Arg Val Thr Asn Asp			
	210	215	220
Asn Ala Ser Cys Arg Leu Glu Lys Gln Ser Arg Leu Cys Met Val Arg			
	225	230	235
Pro Cys Glu Ala Asp Leu Glu Glu Asn Ile Lys Lys Gly Lys Lys Cys			
	245	250	255
Ile Arg Thr Pro Lys Ile Ser Lys Pro Ile Lys Phe Glu Leu Ser Gly			
	260	265	270
Cys Thr Ser Met Lys Thr Tyr Arg Ala Lys Phe Cys Gly Val Cys Thr			
	275	280	285

Asp Gly Arg Cys Cys Thr Pro His Arg Thr Thr Thr Leu Pro Val Glu

290

295

300

Phe Lys Cys Pro Asp Gly Glu Val Met Lys Lys Asn Met Met Phe Ile

305

310

315

320

Lys Thr Cys Ala Cys His Tyr Asn Cys Pro Gly Asp Asn Asp Ile Phe

325

330

335

Glu Ser Leu Tyr Tyr Arg Lys Met Tyr Gly Asp Met Ala

340

345

<210> 83

<211> 2954

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (173).. (1525)

<400> 83

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ggcccagggc gccagggagg ccgcgccggg ctaatccgaa ggggctgcga ggicaggctg 120

taaccgggtc aatgtgtgga atatggggg gctcggctgc agacttggcc aa atg gac 178

Met Asp

1

ggg act att aag gag gct ctg tgc gtg gtg agc gac gac cag tcc ctc 226

Gly Thr Ile Lys Glu Ala Leu Ser Val Val Ser Asp Asp Gln Ser Leu

5

10

15

ttt gac tca gcg tac gga gcg gca gcc cat ctc ccc aag gcc gac atg 274

Phe Asp Ser Ala Tyr Gly Ala Ala Ala His Leu Pro Lys Ala Asp Met

20	25	30	
act gcc tgc ggg agt cct gac tac ggg cag ccc cac aag atc aac ccc	322		
Thr Ala Ser Gly Ser Pro Asp Tyr Gly Gln Pro His Lys Ile Asn Pro			
35	40	45	50
ctc cca cca cag cag gag tgg atc aat cag cca gtc agg gtc aac gtc	370		
Leu Pro Pro Gln Gln Glu Trp Ile Asn Gln Pro Val Arg Val Asn Val			
55	60	65	
aag cgg gag tat gac cac atg aat gga tcc agg gag tct ccg gtc gac	418		
Lys Arg Glu Tyr Asp His Met Asn Gly Ser Arg Glu Ser Pro Val Asp			
70	75	80	
tgc agc gtt agc aaa tgc agc aag ctg gtc ggc gga ggc gag tcc aac	466		
Cys Ser Val Ser Lys Cys Ser Lys Leu Val Gly Gly Gly Glu Ser Asn			
85	90	95	
ccc atg aac tac aac agc tat atg gac gag aag aat ggc ccc cct cct	514		
Pro Met Asn Tyr Asn Ser Tyr Met Asp Glu Lys Asn Gly Pro Pro Pro			
100	105	110	
ccc aac atg acc acc aac gag agg aga gtc atc gtc ccc gca gac ccc	562		
Pro Asn Met Thr Thr Asn Glu Arg Arg Val Ile Val Pro Ala Asp Pro			
115	120	125	130
aca ctg tgg aca cag gag cat gtc agg caa tgg ctg gag tgg gcc ata	610		
Thr Leu Trp Thr Gln Glu His Val Arg Gln Trp Leu Glu Trp Ala Ile			
135	140	145	
aag gag tac agc ttg atg gag atc gac aca tcc ttt ttc cag aac atg	658		
Lys Glu Tyr Ser Leu Met Glu Ile Asp Thr Ser Phe Phe Gln Asn Met			
150	155	160	
gat ggc aag gaa ctg tgt aaa atg aac aag gag gac ttc ctc cgc gcc	706		
Asp Gly Lys Glu Leu Cys Lys Met Asn Lys Glu Asp Phe Leu Arg Ala			

165	170	175	
acc acc ctc tac aac acg gaa gtg ctg ttg tca cac ctc agt tac ctc	754		
Thr Thr Leu Tyr Asn Thr Glu Val Leu Leu Ser His Leu Ser Tyr Leu			
180	185	190	
agg gaa agt tca ctg ctg gcc tat aat aca acc tcc cac acc gac caa	802		
Arg Glu Ser Ser Leu Leu Ala Tyr Asn Thr Thr Ser His Thr Asp Gln			
195	200	205	210
tcc tca cga ttg agt gtc aaa gaa gac cct tct tat gac tca gtc aga	850		
Ser Ser Arg Leu Ser Val Lys Glu Asp Pro Ser Tyr Asp Ser Val Arg			
215	220	225	
aga gga gct tgg ggc aat aac atg aat tct ggc ctc aac aaa agt cct	898		
Arg Gly Ala Trp Gly Asn Asn Met Asn Ser Gly Leu Asn Lys Ser Pro			
230	235	240	
ccc ctt gga ggg gca caa acg atc agt aag aat aca gag caa cgg ccc	946		
Pro Leu Gly Gly Ala Gln Thr Ile Ser Lys Asn Thr Glu Gln Arg Pro			
245	250	255	
cag cca gat ccg tat cag atc ctg ggc ccg acc agc agt cgc cta gcc	994		
Gln Pro Asp Pro Tyr Gln Ile Leu Gly Pro Thr Ser Ser Arg Leu Ala			
260	265	270	
aac cct gga agc ggg cag atc cag ctg tgg caa ttc ctc ctg gag ctg	1042		
Asn Pro Gly Ser Gly Gln Ile Gln Leu Trp Gln Phe Leu Leu Glu Leu			
275	280	285	290
ctc tcc gac agc gcc aac gcc agc tgt atc acc tgg gag ggg acc aac	1090		
Leu Ser Asp Ser Ala Asn Ala Ser Cys Ile Thr Trp Glu Gly Thr Asn			
295	300	305	
ggg gag ttc aaa atg acg gac ccc gat gag gtg gcc agg cgc tgg ggc	1138		

Gly Glu Phe Lys Met Thr Asp Pro Asp Glu Val Ala Arg Arg Trp Gly
 310 315 320
 gag cgg aaa agc aag ccc aac atg aat tac gac aag ctg agc cgg gcc 1186
 Glu Arg Lys Ser Lys Pro Asn Met Asn Tyr Asp Lys Leu Ser Arg Ala
 325 330 335
 ctc cgt tat tac tat gat aaa aac att atg acc aaa gtg cac ggc aaa 1234
 Leu Arg Tyr Tyr Tyr Asp Lys Asn Ile Met Thr Lys Val His Gly Lys
 340 345 350
 aga tat gct tac aaa ttt gac ttc cac ggc att gcc cag gct ctg cag 1282
 Arg Tyr Ala Tyr Lys Phe Asp Phe His Gly Ile Ala Gln Ala Leu Gln
 355 360 365 370
 cca cat ccg acc gag tcg tcc atg tac aag tac cct tct gac atc tcc 1330
 Pro His Pro Thr Glu Ser Ser Met Tyr Lys Tyr Pro Ser Asp Ile Ser
 375 380 385
 tac atg cct tcc caa cat gcc cac cag cag aag gtg aac ttt gtc cct 1378
 Tyr Met Pro Ser Gln His Ala His Gln Gln Lys Val Asn Phe Val Pro
 390 395 400
 ccc cat cca tcc tcc atg cct gtc act tcc tcc agc ttc ttt gga gcc 1426
 Pro His Pro Ser Ser Met Pro Val Thr Ser Ser Ser Phe Phe Gly Ala
 405 410 415
 gca tca caa tac tgg acc tcc acg ggg gga atc tac ccc aac ccc aac 1474
 Ala Ser Gln Tyr Trp Thr Ser Thr Gly Gly Ile Tyr Pro Asn Pro Asn
 420 425 430
 gtc ccc cgc cat cct aac acc cac gtg cct tca cac tta ggc agc tac 1522
 Val Pro Arg His Pro Asn Thr His Val Pro Ser His Leu Gly Ser Tyr
 435 440 445 450
 tac tagaagctta ctcatcagtg gccttctagc tgaagcccat cctgcacact 1575

Tyr

tactggatgc ttggactca acaggacata tgggccttg aaggaagac aaaactggat 1635
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<210> 84

<211> 451

<212> PRT

<213> Homo sapiens

<400> 84

Met Asp Gly Thr Ile Lys Glu Ala Leu Ser Val Val Ser Asp Asp Gln

1 5 10 15

Ser Leu Phe Asp Ser Ala Tyr Gly Ala Ala Ala His Leu Pro Lys Ala

20 25 30

Asp Met Thr Ala Ser Gly Ser Pro Asp Tyr Gly Gln Pro His Lys Ile

35 40 45

Asn Pro Leu Pro Pro Gln Gln Glu Trp Ile Asn Gln Pro Val Arg Val

50 55 60

Asn Val Lys Arg Glu Tyr Asp His Met Asn Gly Ser Arg Glu Ser Pro

65 70 75 80

Val Asp Cys Ser Val Ser Lys Cys Ser Lys Leu Val Gly Gly Gly Glu

85 90 95

Ser Asn Pro Met Asn Tyr Asn Ser Tyr Met Asp Glu Lys Asn Gly Pro

100 105 110

Pro Pro Pro Asn Met Thr Thr Asn Glu Arg Arg Val Ile Val Pro Ala

115 120 125

Asp Pro Thr Leu Trp Thr Gln Glu His Val Arg Gln Trp Leu Glu Trp

130 135 140

Ala Ile Lys Glu Tyr Ser Leu Met Glu Ile Asp Thr Ser Phe Phe Gln

145 150 155 160

Asn Met Asp Gly Lys Glu Leu Cys Lys Met Asn Lys Glu Asp Phe Leu

165 170 175

Arg Ala Thr Thr Leu Tyr Asn Thr Glu Val Leu Leu Ser His Leu Ser

180	185	190	
Tyr Leu Arg Glu Ser Ser Leu Leu Ala Tyr Asn Thr Thr Ser His Thr			
195	200	205	
Asp Gln Ser Ser Arg Leu Ser Val Lys Glu Asp Pro Ser Tyr Asp Ser			
210	215	220	
Val Arg Arg Gly Ala Trp Gly Asn Asn Met Asn Ser Gly Leu Asn Lys			
225	230	235	240
Ser Pro Pro Leu Gly Gly Ala Gln Thr Ile Ser Lys Asn Thr Glu Gln			
245	250	255	
Arg Pro Gln Pro Asp Pro Tyr Gln Ile Leu Gly Pro Thr Ser Ser Arg			
260	265	270	
Leu Ala Asn Pro Gly Ser Gly Gln Ile Gln Leu Trp Gln Phe Leu Leu			
275	280	285	
Glu Leu Leu Ser Asp Ser Ala Asn Ala Ser Cys Ile Thr Trp Glu Gly			
290	295	300	
Thr Asn Gly Glu Phe Lys Met Thr Asp Pro Asp Glu Val Ala Arg Arg			
305	310	315	320
Trp Gly Glu Arg Lys Ser Lys Pro Asn Met Asn Tyr Asp Lys Leu Ser			
325	330	335	
Arg Ala Leu Arg Tyr Tyr Tyr Asp Lys Asn Ile Met Thr Lys Val His			
340	345	350	
Gly Lys Arg Tyr Ala Tyr Lys Phe Asp Phe His Gly Ile Ala Gln Ala			
355	360	365	
Leu Gln Pro His Pro Thr Glu Ser Ser Met Tyr Lys Tyr Pro Ser Asp			
370	375	380	
Ile Ser Tyr Met Pro Ser Gln His Ala His Gln Gln Lys Val Asn Phe			
385	390	395	400

Val Pro Pro His Pro Ser Ser Met Pro Val Thr Ser Ser Ser Phe Phe

405

410

415

Gly Ala Ala Ser Gln Tyr Trp Thr Ser Thr Gly Gly Ile Tyr Pro Asn

420

425

430

Pro Asn Val Pro Arg His Pro Asn Thr His Val Pro Ser His Leu Gly

435

440

445

Ser Tyr Tyr

450

<210> 85

<211> 1817

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (2).. (361)

<400> 85

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1

5

10

15

agg cct gca ggg gat gga acc ttc cag aag tgg gca gct gtg gtg gtg 97

Arg Pro Ala Gly Asp Gly Thr Phe Gln Lys Trp Ala Ala Val Val Val

20

25

30

cct tct gga gag gag cag aga tac acg tgc cat gtg cag cat gag ggg 145

Pro Ser Gly Glu Glu Gln Arg Tyr Thr Cys His Val Gln His Glu Gly

35

40

45

cta ccc gag ccc gtc acc ctg aga tgg aag ccg gct tcc cag ccc acc 193

Leu Pro Glu Pro Val Thr Leu Arg Trp Lys Pro Ala Ser Gln Pro Thr
 50 55 60
 atc ccc aic gtg ggc atc att gct ggc ctg gtt ctc ctt gga tct gtg 241
 Ile Pro Ile Val Gly Ile Ile Ala Gly Leu Val Leu Leu Gly Ser Val
 65 70 75 80
 gtc tct gga gct gtg gtt gct gct gtg ata tgg agg aag aag agc tca 289
 Val Ser Gly Ala Val Val Ala Ala Val Ile Trp Arg Lys Lys Ser Ser
 85 90 95
 ggt gga aaa gga ggg agc tac tct aag gct gag tgg agc gac agt gcc 337
 Gly Gly Lys Gly Gly Ser Tyr Ser Lys Ala Glu Trp Ser Asp Ser Ala
 100 105 110
 cag ggg tct gag tct cac agc ttg taaagcctga gacagctgcc ttgtgtgcga 391
 Gln Gly Ser Glu Ser His Ser Leu
 115 120
 ctgagatgca cagctgcctt gtgtgcgact gagatgcagg atttcctcac gcctccccta 451
 tgtgtcttag gggactctgg ctctctttt tgcaagggcc tctgaatctg tctgtgtccc 511
 tgttagcaca atgtgaggag gtagagaaac agtccacctc tgtgtctacc atgaccccct 571
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 cccatgacct tttaacagca tctgttcat tccctcacc tcccaggct gatctgaggt 1771
 aaactttgaa gtaaaataaa agctgtgttt gagcatcaaa aaaaaa 1817

<210> 86

<211> 120

<212> PRT

<213> Homo sapiens

<400> 86

Gln Gln Asp Gly Glu Gly His Thr Gln Asp Thr Glu Leu Val Glu Thr

1 5 10 15

Arg Pro Ala Gly Asp Gly Thr Phe Gln Lys Trp Ala Ala Val Val Val

20 25 30

Pro Ser Gly Glu Glu Gln Arg Tyr Thr Cys His Val Gln His Glu Gly

35 40 45

Leu Pro Glu Pro Val Thr Leu Arg Trp Lys Pro Ala Ser Gln Pro Thr

50 55 60

Ile Pro Ile Val Gly Ile Ile Ala Gly Leu Val Leu Leu Gly Ser Val

65 70 75 80
 Val Ser Gly Ala Val Val Ala Ala Val Ile Trp Arg Lys Lys Ser Ser
 85 90 95
 Gly Gly Lys Gly Gly Ser Tyr Ser Lys Ala Glu Trp Ser Asp Ser Ala
 100 105 110
 Gln Gly Ser Glu Ser His Ser Leu
 115 120

<210> 87

<211> 2876

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (76).. (1281)

<400> 87

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 tctgagaact tcagg atg cag atg tct cca gcc ctg acc tgc cta gtc ctg 111
 Met Gln Met Ser Pro Ala Leu Thr Cys Leu Val Leu
 1 5 10
 ggc ctg gcc ctt gtc ttt ggt gaa ggg tct gct gtg cac cat ccc cca 159
 Gly Leu Ala Leu Val Phe Gly Glu Gly Ser Ala Val His His Pro Pro
 15 20 25
 tcc tac gtg gcc cac ctg gcc tca gac ttc ggg gtg agg gtg ttt cag 207
 Ser Tyr Val Ala His Leu Ala Ser Asp Phe Gly Val Arg Val Phe Gln
 30 35 40
 cag gtg gcg cag gcc tcc aag gac cgc aac gtg gtt ttc tca ccc tat 255

Gln Val Ala Gln Ala Ser Lys Asp Arg Asn Val Val Phe Ser Pro Tyr
 45 50 55 60
 ggg gtg gcc tcg gtg ttg gcc atg ctc cag ctg aca aca gga gga gaa 303
 Gly Val Ala Ser Val Leu Ala Met Leu Gln Leu Thr Thr Gly Gly Glu
 65 70 75
 acc cag cag cag att caa gca gct atg gga ttc aag att gat gac aag 351
 Thr Gln Gln Gln Ile Gln Ala Ala Met Gly Phe Lys Ile Asp Asp Lys
 80 85 90
 ggc atg gcc ccc gcc ctc cgg cat ctg tac aag gag ctc atg ggg cca 399
 Gly Met Ala Pro Ala Leu Arg His Leu Tyr Lys Glu Leu Met Gly Pro
 95 100 105
 tgg aac aag gat gag atc agc acc aca gac gcg atc ttc gtc cag cgg 447
 Trp Asn Lys Asp Glu Ile Ser Thr Thr Asp Ala Ile Phe Val Gln Arg
 110 115 120
 gat ctg aag ctg gtc cag ggc ttc atg ccc cac ttc ttc agg ctg ttc 495
 Asp Leu Lys Leu Val Gln Gly Phe Met Pro His Phe Phe Arg Leu Phe
 125 130 135 140
 cgg agc acg gtc aag caa gtg gac ttt tca gag gtg gag aga gcc aga 543
 Arg Ser Thr Val Lys Gln Val Asp Phe Ser Glu Val Glu Arg Ala Arg
 145 150 155
 ttc atc atc aat gac tgg gtg aag aca cac aca aaa ggt atg atc agc 591
 Phe Ile Ile Asn Asp Trp Val Lys Thr His Thr Lys Gly Met Ile Ser
 160 165 170
 aac ttg ctt ggg aaa gga gcc gtg gac cag ctg aca cgg ctg gtg ctg 639
 Asn Leu Leu Gly Lys Gly Ala Val Asp Gln Leu Thr Arg Leu Val Leu
 175 180 185
 gtg aat gcc ctc tac ttc aac ggc cag tgg aag act ccc ttc ccc gac 687

Val Asn Ala Leu Tyr Phe Asn Gly Gln Trp Lys Thr Pro Phe Pro Asp
 190 195 200
 tcc agc acc cac cgc cgc ctc ttc cac aaa tca gac ggc agc act gtc 735
 Ser Ser Thr His Arg Arg Leu Phe His Lys Ser Asp Gly Ser Thr Val
 205 210 215 220
 tct gtg ccc atg atg gct cag acc aac aag ttc aac tat act gag ttc 783
 Ser Val Pro Met Met Ala Gln Thr Asn Lys Phe Asn Tyr Thr Glu Phe
 225 230 235
 acc acg ccc gat ggc cat tac tac gac atc ctg gaa ctg ccc tac cac 831
 Thr Thr Pro Asp Gly His Tyr Tyr Asp Ile Leu Glu Leu Pro Tyr His
 240 245 250
 ggg gac acc ctc agc atg ttc att gct gcc cct tat gaa aaa gag gtg 879
 Gly Asp Thr Leu Ser Met Phe Ile Ala Ala Pro Tyr Glu Lys Glu Val
 255 260 265
 cct ctc tct gcc ctc acc aac att ctg agt gcc cag ctc atc agc cac 927
 Pro Leu Ser Ala Leu Thr Asn Ile Leu Ser Ala Gln Leu Ile Ser His
 270 275 280
 tgg aaa ggc aac atg acc agg ctg ccc cgc ctc ctg gtt ctg ccc aag 975
 Trp Lys Gly Asn Met Thr Arg Leu Pro Arg Leu Leu Val Leu Pro Lys
 285 290 295 300
 ttc tcc ctg gag act gaa gtc gac ctc agg aag ccc cta gag aac ctg 1023
 Phe Ser Leu Glu Thr Glu Val Asp Leu Arg Lys Pro Leu Glu Asn Leu
 305 310 315
 gga atg acc gac atg ttc aga cag ttt cag gct gac ttc acg agt ctt 1071
 Gly Met Thr Asp Met Phe Arg Gln Phe Gln Ala Asp Phe Thr Ser Leu
 320 325 330

tca gac caa gag cct ctc cac gtc gcg cag gcg ctg cag aaa gtg aag 1119

Ser Asp Gln Glu Pro Leu His Val Ala Gln Ala Leu Gln Lys Val Lys

335

340

345

atc gag gig aac gag agt ggc acg gtg gcc tcc tca tcc aca gct gtc 1167

Ile Glu Val Asn Glu Ser Gly Thr Val Ala Ser Ser Ser Thr Ala Val

350

355

360

ata gtc tca gcc cgc atg gcc ccc gag gag atc atc atg gac aga ccc 1215

Ile Val Ser Ala Arg Met Ala Pro Glu Glu Ile Ile Met Asp Arg Pro

365

370

375

380

ttc ctc ttt gtg gtc cgg cac aac ccc aca gga aca gtc ctt ttc atg 1263

Phe Leu Phe Val Val Arg His Asn Pro Thr Gly Thr Val Leu Phe Met

385

390

395

ggc caa gtg atg gaa ccc tgacctggg gaaagacgcc ttcactggg 1311

Gly Gln Val Met Glu Pro

400

acaaaacigg agatgcatcg ggaaagaaga aactccgaag aaaagaattt tagtgitaat 1371

gactctttct gaaggaagag aagacatttg ccttttgta aaagatggta aaccagatct 1431

gctccaaga ccttggccctc tccttgagg accttaggt caaacccct agtctccacc 1491

tgagacctg ggagagaagt ttgaagcaca actcccttaa ggtciccaaa ccagacggtg 1551

acgcctgcgg gacctcigg ggcacctgct tccaccgctc tctctgcca ctcgggctg 1611

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gccaccgcgg aggaggctgg tgacaggcca aaggccagtg gaagaaacac ctttcalct 1791

cagagtccac tgtggcactg gccaccctc cccagtacag gggctctgca ggtggcagag 1851

tgaatgtccc ccatcatgig gcccaactct cctggccigg ccatctccct cccagaaac 1911

agtgctcag ggttatttg gagtgtaggt gacttgta ctcattgaag cagattctg 1971

cttcctttta tttttatagg aatagaggaa gaaatgicag atgcgtgccc agctcttcac 2031

cccccaatct ctgttggtggg aggggigtac ctaaataitt atcatatcct tgccttgag 2091
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 atatataat tttaaatata cttaaatata ttttctaata atctttaaat atatataat 2811
 attttaaaga ccaatttaig ggagaattgc acacagatgt gaaatgaatg taatctaata 2871
 gaagc 2876

<210> 88

<211> 402

<212> PRT

<213> Homo sapiens

<400> 88

Met Gln Met Ser Pro Ala Leu Thr Cys Leu Val Leu Gly Leu Ala Leu
 Val Phe Gly Glu Gly Ser Ala Val His His Pro Pro Ser Tyr Val Ala
 1 5 10 15
 His Leu Ala Ser Asp Phe Gly Val Arg Val Phe Gln Gln Val Ala Gln
 20 25 30
 Ala Ser Lys Asp Arg Asn Val Val Phe Ser Pro Tyr Gly Val Ala Ser

35	40	45	
Val Leu Ala Met Leu Gln Leu Thr Thr Gly Gly Glu Thr Gln Gln Gln			
50	55	60	
Ile Gln Ala Ala Met Gly Phe Lys Ile Asp Asp Lys Gly Met Ala Pro			
65	70	75	80
Ala Leu Arg His Leu Tyr Lys Glu Leu Met Gly Pro Trp Asn Lys Asp			
85	90	95	
Glu Ile Ser Thr Thr Asp Ala Ile Phe Val Gln Arg Asp Leu Lys Leu			
100	105	110	
Val Gln Gly Phe Met Pro His Phe Phe Arg Leu Phe Arg Ser Thr Val			
115	120	125	
Lys Gln Val Asp Phe Ser Glu Val Glu Arg Ala Arg Phe Ile Ile Asn			
130	135	140	
Asp Trp Val Lys Thr His Thr Lys Gly Met Ile Ser Asn Leu Leu Gly			
145	150	155	160
Lys Gly Ala Val Asp Gln Leu Thr Arg Leu Val Leu Val Asn Ala Leu			
165	170	175	
Tyr Phe Asn Gly Gln Trp Lys Thr Pro Phe Pro Asp Ser Ser Thr His			
180	185	190	
Arg Arg Leu Phe His Lys Ser Asp Gly Ser Thr Val Ser Val Pro Met			
195	200	205	
Met Ala Gln Thr Asn Lys Phe Asn Tyr Thr Glu Phe Thr Thr Pro Asp			
210	215	220	
Gly His Tyr Tyr Asp Ile Leu Glu Leu Pro Tyr His Gly Asp Thr Leu			
225	230	235	240
Ser Met Phe Ile Ala Ala Pro Tyr Glu Lys Glu Val Pro Leu Ser Ala			

245 250 255
Leu Thr Asn Ile Leu Ser Ala Gln Leu Ile Ser His Trp Lys Gly Asn
260 265 270
Met Thr Arg Leu Pro Arg Leu Leu Val Leu Pro Lys Phe Ser Leu Glu
275 280 285
Thr Glu Val Asp Leu Arg Lys Pro Leu Glu Asn Leu Gly Met Thr Asp
290 295 300
Met Phe Arg Gln Phe Gln Ala Asp Phe Thr Ser Leu Ser Asp Gln Glu
305 310 315 320
Pro Leu His Val Ala Gln Ala Leu Gln Lys Val Lys Ile Glu Val Asn
325 330 335
Glu Ser Gly Thr Val Ala Ser Ser Ser Thr Ala Val Ile Val Ser Ala
340 345 350
Arg Met Ala Pro Glu Glu Ile Ile Met Asp Arg Pro Phe Leu Phe Val
355 360 365
Val Arg His Asn Pro Thr Gly Thr Val Leu Phe Met Gly Gln Val Met
370 375 380
Glu Pro
385

<210> 89

<211> 1412

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (52).. (1341)

<400> 89

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Met Ser

1

ttc acc act cgc tcc acc ttc tcc acc aac tac cgg tcc ctg ggc tct 105

Phe Thr Thr Arg Ser Thr Phe Ser Thr Asn Tyr Arg Ser Leu Gly Ser

5

10

15

gtc cag gcg ccc agc tac ggc gcc cgg ccg gtc agc agc gcg gcc agc 153

Val Gln Ala Pro Ser Tyr Gly Ala Arg Pro Val Ser Ser Ala Ala Ser

20

25

30

gtc tat gca ggc gct ggg ggc tct ggt tcc cgg atc tcc gtg tcc cgc 201

Val Tyr Ala Gly Ala Gly Gly Ser Gly Ser Arg Ile Ser Val Ser Arg

35

40

45

50

tcc acc agc ttc agg ggc ggc atg ggg tcc ggg ggc ctg gcc acc ggg 249

Ser Thr Ser Phe Arg Gly Gly Met Gly Ser Gly Gly Leu Ala Thr Gly

55

60

65

ata gcc ggg ggt ctg gca gga atg gga ggc atc cag aac gag aag gag 297

Ile Ala Gly Gly Leu Ala Gly Met Gly Gly Ile Gln Asn Glu Lys Glu

70

75

80

acc atg caa agc ctg aac gac cgc ctg gcc tct tac ctg gac aga gtg 345

Thr Met Gln Ser Leu Asn Asp Arg Leu Ala Ser Tyr Leu Asp Arg Val

85

90

95

agg agc ctg gag acc gag aac cgg agg ctg gag agc aaa atc cgg gag 393

Arg Ser Leu Glu Thr Glu Asn Arg Arg Leu Glu Ser Lys Ile Arg Glu

100

105

110

cac ttg gag aag aag gga ccc cag gtc aga gac tgg agc cat tac ttc 441

His Leu Glu Lys Lys Gly Pro Gln Val Arg Asp Trp Ser His Tyr Phe

115	120	125	130	
aag atc atc gag gac ctg agg gct cag atc ttc gca aat act gtg gac	489			
Lys Ile Ile Glu Asp Leu Arg Ala Gln Ile Phe Ala Asn Thr Val Asp				
	135	140	145	
aat gcc cgc atc gtt ctg cag att gac aat gcc cgt ctt gct gct gat	537			
Asn Ala Arg Ile Val Leu Gln Ile Asp Asn Ala Arg Leu Ala Ala Asp				
	150	155	160	
gac ttt aga gtc aag tat gag aca gag ctg gcc atg cgc cag tct gtg	585			
Asp Phe Arg Val Lys Tyr Glu Thr Glu Leu Ala Met Arg Gln Ser Val				
	165	170	175	
gag aac gac atc cat ggg ctc cgc aag gtc att gat gac acc aat atc	633			
Glu Asn Asp Ile His Gly Leu Arg Lys Val Ile Asp Asp Thr Asn Ile				
	180	185	190	
aca cga ctg cag ctg gag aca gag atc gag gct ctc aag gag gag ctg	681			
Thr Arg Leu Gln Leu Glu Thr Glu Ile Glu Ala Leu Lys Glu Glu Leu				
	195	200	205	210
ctc ttc atg aag aag aac cac gaa gag gaa gta aaa ggc cta caa gcc	729			
Leu Phe Met Lys Lys Asn His Glu Glu Glu Val Lys Gly Leu Gln Ala				
	215	220	225	
cag att gcc agc tct ggg ttg acc gtg gag gta gat gcc ccc aaa tct	777			
Gln Ile Ala Ser Ser Gly Leu Thr Val Glu Val Asp Ala Pro Lys Ser				
	230	235	240	
cag gac ctc gcc aag atc atg gca gac atc cgg gcc caa tat gac gag	825			
Gln Asp Leu Ala Lys Ile Met Ala Asp Ile Arg Ala Gln Tyr Asp Glu				
	245	250	255	
ctg gct cgg aag aac cga gag gag cta gac aag tac tgg tct cag cag	873			

Leu Ala Arg Lys Asn Arg Glu Glu Leu Asp Lys Tyr Trp Ser Gln Gln
 260 265 270
 att gag gag agc acc aca gtg gtc acc aca cag tct gct gag gtt gga 921
 Ile Glu Glu Ser Thr Thr Val Val Thr Thr Gln Ser Ala Glu Val Gly
 275 280 285 290
 gct gct gag acg acg ctc aca gag ctg aga cgt aca gtc cag tcc ttg 969
 Ala Ala Glu Thr Thr Leu Thr Glu Leu Arg Arg Thr Val Gln Ser Leu
 295 300 305
 gag atc gac ctg gac tcc atg aga aat ctg aag gcc agc ttg gag aac 1017
 Glu Ile Asp Leu Asp Ser Met Arg Asn Leu Lys Ala Ser Leu Glu Asn
 310 315 320
 agc ctg agg gag gtg gag gcc cgc tac gcc cta cag atg gag cag ctc 1065
 Ser Leu Arg Glu Val Glu Ala Arg Tyr Ala Leu Gln Met Glu Gln Leu
 325 330 335
 aac ggg atc ctg ctg cac ctt gag tca gag ctg gca cag acc cgg gca 1113
 Asn Gly Ile Leu Leu His Leu Glu Ser Glu Leu Ala Gln Thr Arg Ala
 340 345 350
 gag gga cag cgc cag gcc cag gag tat gag gcc ctg ctg aac atc aag 1161
 Glu Gly Gln Arg Gln Ala Gln Glu Tyr Glu Ala Leu Leu Asn Ile Lys
 355 360 365 370
 gtc aag ctg gag gct gag atc gcc acc tac cgc cgc ctg ctg gaa gat 1209
 Val Lys Leu Glu Ala Glu Ile Ala Thr Tyr Arg Arg Leu Leu Glu Asp
 375 380 385
 ggc gag gac ttt aat ctt ggt gat gcc ttg gac agc agc aac tcc atg 1257
 Gly Glu Asp Phe Asn Leu Gly Asp Ala Leu Asp Ser Ser Asn Ser Met
 390 395 400
 caa acc atc caa aag acc acc acc cgc cgg ata gtg gat ggc aaa gtg 1305

Gln Thr Ile Gln Lys Thr Thr Thr Arg Arg Ile Val Asp Gly Lys Val

405

410

415

gtg tct gag acc aat gac acc aaa gtt ctg agg cat taagccagca 1351

Val Ser Glu Thr Asn Asp Thr Lys Val Leu Arg His

420

425

430

gaagcagggt accctttggg gagcaggagg ccaataaaaa gttcagagtt cattggatgt 1411

c

1412

<210> 90

<211> 430

<212> PRT

<213> Homo sapiens

<400> 90

Met Ser Phe Thr Thr Arg Ser Thr Phe Ser Thr Asn Tyr Arg Ser Leu

1

5

10

15

Gly Ser Val Gln Ala Pro Ser Tyr Gly Ala Arg Pro Val Ser Ser Ala

20

25

30

Ala Ser Val Tyr Ala Gly Ala Gly Gly Ser Gly Ser Arg Ile Ser Val

35

40

45

Ser Arg Ser Thr Ser Phe Arg Gly Gly Met Gly Ser Gly Gly Leu Ala

50

55

60

Thr Gly Ile Ala Gly Gly Leu Ala Gly Met Gly Gly Ile Gln Asn Glu

65

70

75

80

Lys Glu Thr Met Gln Ser Leu Asn Asp Arg Leu Ala Ser Tyr Leu Asp

85

90

95

Arg Val Arg Ser Leu Glu Thr Glu Asn Arg Arg Leu Glu Ser Lys Ile

100

105

110

Arg Glu His Leu Glu Lys Lys Gly Pro Gln Val Arg Asp Trp Ser His
115 120 125
Tyr Phe Lys Ile Ile Glu Asp Leu Arg Ala Gln Ile Phe Ala Asn Thr
130 135 140
Val Asp Asn Ala Arg Ile Val Leu Gln Ile Asp Asn Ala Arg Leu Ala
145 150 155 160
Ala Asp Asp Phe Arg Val Lys Tyr Glu Thr Glu Leu Ala Met Arg Gln
165 170 175
Ser Val Glu Asn Asp Ile His Gly Leu Arg Lys Val Ile Asp Asp Thr
180 185 190
Asn Ile Thr Arg Leu Gln Leu Glu Thr Glu Ile Glu Ala Leu Lys Glu
195 200 205
Glu Leu Leu Phe Met Lys Lys Asn His Glu Glu Glu Val Lys Gly Leu
210 215 220
Gln Ala Gln Ile Ala Ser Ser Gly Leu Thr Val Glu Val Asp Ala Pro
225 230 235 240
Lys Ser Gln Asp Leu Ala Lys Ile Met Ala Asp Ile Arg Ala Gln Tyr
245 250 255
Asp Glu Leu Ala Arg Lys Asn Arg Glu Glu Leu Asp Lys Tyr Trp Ser
260 265 270
Gln Gln Ile Glu Glu Ser Thr Thr Val Val Thr Thr Gln Ser Ala Glu
275 280 285
Val Gly Ala Ala Glu Thr Thr Leu Thr Glu Leu Arg Arg Thr Val Gln
290 295 300
Ser Leu Glu Ile Asp Leu Asp Ser Met Arg Asn Leu Lys Ala Ser Leu
305 310 315 320

Glu Asn Ser Leu Arg Glu Val Glu Ala Arg Tyr Ala Leu Gln Met Glu

325

330

335

Gln Leu Asn Gly Ile Leu Leu His Leu Glu Ser Glu Leu Ala Gln Thr

340

345

350

Arg Ala Glu Gly Gln Arg Gln Ala Gln Glu Tyr Glu Ala Leu Leu Asn

355

360

365

Ile Lys Val Lys Leu Glu Ala Glu Ile Ala Thr Tyr Arg Arg Leu Leu

370

375

380

Glu Asp Gly Glu Asp Phe Asn Leu Gly Asp Ala Leu Asp Ser Ser Asn

385

390

395

400

Ser Met Gln Thr Ile Gln Lys Thr Thr Thr Arg Arg Ile Val Asp Gly

405

410

415

Lys Val Val Ser Glu Thr Asn Asp Thr Lys Val Leu Arg His

420

425

430

<210> 91

<211> 1040

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (171).. (968)

<400> 91

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ttctttgaag gagatgctaa gtttggggaa agaaacgaag ggagcggaca aggaggagaa 120

gg tgcctgaa tgggaacccc ccgaagcgcc tgaaaaggag agacaggagg atg atg 176

Met Met

1

tcc cag ctg gag ctg ctg agt ggg gga gag atg ctg tgc ggt ggc ttc 224
 Ser Gln Leu Glu Leu Leu Ser Gly Gly Glu Met Leu Cys Gly Gly Phe
 5 10 15
 tac cct cgg ctg tcc tgc tgc ctg cgg agt gac agc ccg ggg cta ggg 272
 Tyr Pro Arg Leu Ser Cys Cys Leu Arg Ser Asp Ser Pro Gly Leu Gly
 20 25 30
 cgc ctg gag aat aag ata ttt tct gtt acc aac aac aca gaa tgt ggg 320
 Arg Leu Glu Asn Lys Ile Phe Ser Val Thr Asn Asn Thr Glu Cys Gly
 35 40 45 50
 aag tta ctg gag gaa atc aaa tgt gca ctt tgc tct cca cat tct caa 368
 Lys Leu Leu Glu Glu Ile Lys Cys Ala Leu Cys Ser Pro His Ser Gln
 55 60 65
 agc ctg ttc cac tca cct gag aga gaa gtc ttg gaa aga gac cta gta 416
 Ser Leu Phe His Ser Pro Glu Arg Glu Val Leu Glu Arg Asp Leu Val
 70 75 80
 ctt cct ctg ctg tgc aaa gac tat tgc aaa gaa ttc tti tac act tgc 464
 Leu Pro Leu Leu Cys Lys Asp Tyr Cys Lys Glu Phe Phe Tyr Thr Cys
 85 90 95
 cga ggc cat att cca ggt ttc ctt caa aca act gcg gat gag ttt tgc 512
 Arg Gly His Ile Pro Gly Phe Leu Gln Thr Thr Ala Asp Glu Phe Cys
 100 105 110
 ttt tac tat gca aga aaa gat ggt ggg ttg tgc ttt cca gat ttt cca 560
 Phe Tyr Tyr Ala Arg Lys Asp Gly Gly Leu Cys Phe Pro Asp Phe Pro
 115 120 125 130
 aga aaa caa gtc aga gga cca gca tct aac tac ttg gac cag atg gaa 608
 Arg Lys Gln Val Arg Gly Pro Ala Ser Asn Tyr Leu Asp Gln Met Glu

135	140	145	
gaa tat gac aaa gtg gaa gag atc agc aga aag cac aaa cac aac tgc			656
Glu Tyr Asp Lys Val Glu Glu Ile Ser Arg Lys His Lys His Asn Cys			
150	155	160	
ttc tgt att cag gag gtt gtg agt ggg ctg cgg cag ccc gtt ggt gcc			704
Phe Cys Ile Gln Glu Val Val Ser Gly Leu Arg Gln Pro Val Gly Ala			
165	170	175	
ctg cat agt ggg gat ggc tgc caa cgt ctc ttc att ctg gaa aaa gaa			752
Leu His Ser Gly Asp Gly Ser Gln Arg Leu Phe Ile Leu Glu Lys Glu			
180	185	190	
ggt tat gtg aag ata ctt acc cct gaa gga gaa att ttc aag gag cct			800
Gly Tyr Val Lys Ile Leu Thr Pro Glu Gly Glu Ile Phe Lys Glu Pro			
195	200	205	210
tat ttg gac att cac aaa ctt gtt caa agt gga ata aag gtt ggc ttt			848
Tyr Leu Asp Ile His Lys Leu Val Gln Ser Gly Ile Lys Val Gly Phe			
215	220	225	
tta aat ttt att tat ttt tgt gct ggc tac gtt aat ttt att tta gtg			896
Leu Asn Phe Ile Tyr Phe Cys Ala Gly Tyr Val Asn Phe Ile Leu Val			
230	235	240	
tta cct tcc tca ctg aag gta ttt ctt tgt aat aaa aga aag aat ctt			944
Leu Pro Ser Ser Leu Lys Val Phe Leu Cys Asn Lys Arg Lys Asn Leu			
245	250	255	
gca gga gaa aat aag ggg gca aca taagaaacaa taattatggc acctgaatta			998
Ala Gly Glu Asn Lys Gly Ala Thr			
260	265		
ggacagtgc attaaakgtt ggctktttaw attttaaaaa aa			1040

<210> 92

<211> 266

<212> PRT

<213> Homo sapiens

<400> 92

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Gly Phe Tyr Pro Arg Leu Ser Cys Cys Leu Arg Ser Asp Ser Pro Gly

20 25 30

Leu Gly Arg Leu Glu Asn Lys Ile Phe Ser Val Thr Asn Asn Thr Glu

35 40 45

Cys Gly Lys Leu Leu Glu Glu Ile Lys Cys Ala Leu Cys Ser Pro His

50 55 60

Ser Gln Ser Leu Phe His Ser Pro Glu Arg Glu Val Leu Glu Arg Asp

65 70 75 80

Leu Val Leu Pro Leu Leu Cys Lys Asp Tyr Cys Lys Glu Phe Phe Tyr

85 90 95

Thr Cys Arg Gly His Ile Pro Gly Phe Leu Gln Thr Thr Ala Asp Glu

100 105 110

Phe Cys Phe Tyr Tyr Ala Arg Lys Asp Gly Gly Leu Cys Phe Pro Asp

115 120 125

Phe Pro Arg Lys Gln Val Arg Gly Pro Ala Ser Asn Tyr Leu Asp Gln

130 135 140

Met Glu Glu Tyr Asp Lys Val Glu Glu Ile Ser Arg Lys His Lys His

145 150 155 160

Asn Cys Phe Cys Ile Gln Glu Val Val Ser Gly Leu Arg Gln Pro Val

165 170 175
 Gly Ala Leu His Ser Gly Asp Gly Ser Gln Arg Leu Phe Ile Leu Glu
 180 185 190
 Lys Glu Gly Tyr Val Lys Ile Leu Thr Pro Glu Gly Glu Ile Phe Lys
 195 200 205
 Glu Pro Tyr Leu Asp Ile His Lys Leu Val Gln Ser Gly Ile Lys Val
 210 215 220
 Gly Phe Leu Asn Phe Ile Tyr Phe Cys Ala Gly Tyr Val Asn Phe Ile
 225 230 235 240
 Leu Val Leu Pro Ser Ser Leu Lys Val Phe Leu Cys Asn Lys Arg Lys
 245 250 255
 Asn Leu Ala Gly Glu Asn Lys Gly Ala Thr
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<210> 93

<211> 1639

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (75).. (371)

<400> 93

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 Met Thr Ser Lys Leu Ala Val Ala Leu Leu Ala Ala
 1 5 10
 ttc ctg att tct gca gct ctg tgt gaa ggt gca gtt ttg cca agg agt 158

Phe Leu Ile Ser Ala Ala Leu Cys Glu Gly Ala Val Leu Pro Arg Ser
 15 20 25
 gct aaa gaa ctt aga tgt cag tgc ata aag aca tac tcc aaa cct ttc 206
 Ala Lys Glu Leu Arg Cys Gln Cys Ile Lys Thr Tyr Ser Lys Pro Phe
 30 35 40
 cac ccc aaa ttt atc aaa gaa ctg aga gtg att gag agt gga cca cac 254
 His Pro Lys Phe Ile Lys Glu Leu Arg Val Ile Glu Ser Gly Pro His
 45 50 55 60
 tgc gcc aac aca gaa att att gta aag ctt tct gat gga aga gag ctc 302
 Cys Ala Asn Thr Glu Ile Ile Val Lys Leu Ser Asp Gly Arg Glu Leu
 65 70 75
 tgt ctg gac ccc aag gaa aac tgg gtg cag agg gtt gtg gag aag ttt 350
 Cys Leu Asp Pro Lys Glu Asn Trp Val Gln Arg Val Val Glu Lys Phe
 80 85 90
 ttg aag agg gct gag aat tca taaaaaatt cattctctgt ggtatccaag 401
 Leu Lys Arg Ala Glu Asn Ser
 95
 aatcagtga gatgccagt aaacttcaag caaatctact tcaacacttc atgtattgtg 461
 tgggtctgtt gtagggttgc cagatgcaat acaagattcc tggttaaatt tgaatttcag 521
 taaacaatga atagtitttc attgtaccat gaaatatcca gaacatactt atatgtaaag 581
 tattatttat ttgaatctac aaaaaacaac aaataatttt taaatataag gattttccta 641
 gatattgcac gggagaatat acaaatagca aaattgagcc aaggccaag agaatatccg 701
 aactttaatt tcaggaattg aatgggtttg ctagaatgtg atatttgaag catcacataa 761
 aaatgatggg acaataaatt ttgccataaa gtcaaattta gctggaaatc ctggattttt 821
 ttctgtttaa tctggcaacc ctagtctgct agccaggatc cacaagtcct tgttccactg 881
 tgccttgggt tctccittat ttctaagtgg aaaaagtatt agccaccatc ttacctcaca 941
 gigtatgtgt gaggacatgt ggaagcactt taagtitttt catcataaca taaattattt 1001

tcaagtgtaa cttattaacc tatttattat ttatgtattt atttaagcat caaatatttg 1061
 tgcaagaatt lggaaaaaa gaagatgaat catlgaatga atagttataa agaigtata 1121
 gtaaaattat tttattttag atattaaatg atgttttatt agataaatit caatcagggt 1181
 tttlagatta aacaaagaaa caatlgggta cccagttaaa tttcatitc agataaaca 1241
 caaataattt tttagtataa gtacattatt gtttatctga aagttttaat tgaactaaca 1301
 atccitagttt gatactccca gctctgcat tgcagcgtt gttggtagtg ctgtgttgaa 1361
 ttacggaata atgagttaga actattaaaa cagccaaaac tccacagica atattagtaa 1421
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 tgactgcatt tttaaalaca aggttttata tttttaactt taagatgttt ttatgtgctc 1541
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 aaaatataat ttgttgtcaa agtaaaaaaa aaaaaaaa 1639

<210> 94

<211> 99

<212> PRT

<213> Homo sapiens

<400> 94

Met	Thr	Ser	Lys	Leu	Ala	Val	Ala	Leu	Leu	Ala	Ala	Phe	Leu	Ile	Ser
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1				5					10					15	
Arg	Cys	Gln	Cys	Ile	Lys	Thr	Tyr	Ser	Lys	Pro	Phe	His	Pro	Lys	Phe
				20					25					30	
Ile	Lys	Glu	Leu	Arg	Val	Ile	Glu	Ser	Gly	Pro	His	Cys	Ala	Asn	Thr
				35					40					45	
Glu	Ile	Ile	Val	Lys	Leu	Ser	Asp	Gly	Arg	Glu	Leu	Cys	Leu	Asp	Pro
				50					55					60	
Lys	Glu	Asn	Trp	Val	Gln	Arg	Val	Val	Glu	Lys	Phe	Leu	Lys	Arg	Ala

Gly Gln Gly Gln Ser Glu Pro Gly Glu Tyr Glu Gln Arg Leu Ser Leu
 80 85 90
 cag gac aga ggg gct act ctg gcc ctg act caa gtc acc ccc caa gac 337
 Gln Asp Arg Gly Ala Thr Leu Ala Leu Thr Gln Val Thr Pro Gln Asp
 95 100 105 110
 gag cgc atc ttc ttg tgc cag ggc aag cgc cct cgg tcc cag gag tac 385
 Glu Arg Ile Phe Leu Cys Gln Gly Lys Arg Pro Arg Ser Gln Glu Tyr
 115 120 125
 cgc atc cag ctc cgc gtc tac aaa gct ccg gag gag cca aac atc cag 433
 Arg Ile Gln Leu Arg Val Tyr Lys Ala Pro Glu Glu Pro Asn Ile Gln
 130 135 140
 gtc aac ccc ctg ggc atc cct gtg aac agt aag gag cct gag gag gtc 481
 Val Asn Pro Leu Gly Ile Pro Val Asn Ser Lys Glu Pro Glu Glu Val
 145 150 155
 gct acc tgt gta ggg agg aac ggg tac ccc att cct caa gtc atc tgg 529
 Ala Thr Cys Val Gly Arg Asn Gly Tyr Pro Ile Pro Gln Val Ile Trp
 160 165 170
 tac aag aat ggc cgg cct ctg aag gag gag aag aac cgg gtc cac att 577
 Tyr Lys Asn Gly Arg Pro Leu Lys Glu Glu Lys Asn Arg Val His Ile
 175 180 185 190
 cag tgc tcc cag act gtg gag tgc agt ggt ttg tac acc ttg cag agt 625
 Gln Ser Ser Gln Thr Val Glu Ser Ser Gly Leu Tyr Thr Leu Gln Ser
 195 200 205
 att ctg aag gca cag ctg gtt aaa gaa gac aaa gat gcc cag ttt tac 673
 Ile Leu Lys Ala Gln Leu Val Lys Glu Asp Lys Asp Ala Gln Phe Tyr
 210 215 220

tgt gag ctc aac tac cgg ctg ccc agt ggg aac cac atg aag gag tcc	721
Cys Glu Leu Asn Tyr Arg Leu Pro Ser Gly Asn His Met Lys Glu Ser	
225 230 235	
agg gaa gtc acc gtc cct gtt ttc tac ccg aca gaa aaa gtg tgg ctg	769
Arg Glu Val Thr Val Pro Val Phe Tyr Pro Thr Glu Lys Val Trp Leu	
240 245 250	
gaa gtg gag ccc gtg gga atg ctg aag gaa ggg gac cgc gtg gaa atc	817
Glu Val Glu Pro Val Gly Met Leu Lys Glu Gly Asp Arg Val Glu Ile	
255 260 265 270	
agg tgt ttg gct gat ggc aac cct cca cca cac ttc agc atc agc aag	865
Arg Cys Leu Ala Asp Gly Asn Pro Pro Pro His Phe Ser Ile Ser Lys	
275 280 285	
cag aac ccc agc acc agg gag gca gag gaa gag aca acc aac gac aac	913
Gln Asn Pro Ser Thr Arg Glu Ala Glu Glu Glu Thr Thr Asn Asp Asn	
290 295 300	
ggg gtc ctg gtg ctg gag cct gcc cgg aag gaa cac agt ggg cgc tat	961
Gly Val Leu Val Leu Glu Pro Ala Arg Lys Glu His Ser Gly Arg Tyr	
305 310 315	
gaa tgt cag gcc tgg aac ttg gac acc atg ata tcg ctg ctg agt gaa	1009
Glu Cys Gln Ala Trp Asn Leu Asp Thr Met Ile Ser Leu Leu Ser Glu	
320 325 330	
cca cag gaa cta ctg gtg aac tat gtg tct gac gtc cga gtg agt ccc	1057
Pro Gln Glu Leu Leu Val Asn Tyr Val Ser Asp Val Arg Val Ser Pro	
335 340 345 350	
gca gcc cct gag aga cag gaa ggc agc agc ctc acc ctg acc tgt gag	1105
Ala Ala Pro Glu Arg Gln Glu Gly Ser Ser Leu Thr Leu Thr Cys Glu	
355 360 365	

gca gag agt agc cag gac ctc gag ttc cag tgg ctg aga gaa gag aca 1153
 Ala Glu Ser Ser Gln Asp Leu Glu Phe Gln Trp Leu Arg Glu Glu Thr
 370 375 380
 gac cag gtg ctg gaa agg ggg cct gtg ctt cag ttg cat gac ctg aaa 1201
 Asp Gln Val Leu Glu Arg Gly Pro Val Leu Gln Leu His Asp Leu Lys
 385 390 395
 cgg gag gca gga ggc ggc tat cgc tgc gtg gcg tct gtg ccc agc ata 1249
 Arg Glu Ala Gly Gly Gly Tyr Arg Cys Val Ala Ser Val Pro Ser Ile
 400 405 410
 ccc ggc ctg aac cgc aca cag ctg gtc aag ctg gcc att ttt ggc ccc 1297
 Pro Gly Leu Asn Arg Thr Gln Leu Val Lys Leu Ala Ile Phe Gly Pro
 415 420 425 430
 cct tgg atg gca ttc aag gag agg aag gtg tgg gtg aaa gag aat atg 1345
 Pro Trp Met Ala Phe Lys Glu Arg Lys Val Trp Val Lys Glu Asn Met
 435 440 445
 gtg tlg aat ctg tct tgt gaa gcg tca ggg cac ccc cgg ccc acc atc 1393
 Val Leu Asn Leu Ser Cys Glu Ala Ser Gly His Pro Arg Pro Thr Ile
 450 455 460
 tcc tgg aac gtc aac ggc acg gca agt gaa caa gac caa gat cca cag 1441
 Ser Trp Asn Val Asn Gly Thr Ala Ser Glu Gln Asp Gln Asp Pro Gln
 465 470 475
 cga gtc ctg agc acc ctg aat gtc ctc gtg acc ccg gag ctg ttg gag 1489
 Arg Val Leu Ser Thr Leu Asn Val Leu Val Thr Pro Glu Leu Leu Glu
 480 485 490
 aca ggt gtt gaa tgc acg gcc tcc aac gac ctg ggc aaa aac acc agc 1537
 Thr Gly Val Glu Cys Thr Ala Ser Asn Asp Leu Gly Lys Asn Thr Ser

495 500 505 510
 atc ctc ttc ctg gag ctg gtc aat tta acc acc ctc aca cca gac tcc 1585
 Ile Leu Phe Leu Glu Leu Val Asn Leu Thr Thr Leu Thr Pro Asp Ser
 515 520 525
 aac aca acc act ggc ctc agc act tcc act gcc agt cct cat acc aga 1633
 Asn Thr Thr Thr Gly Leu Ser Thr Ser Thr Ala Ser Pro His Thr Arg
 530 535 540
 gcc aac agc acc tcc aca gag aga aag ctg ccg gag ccg gag agc cgg 1681
 Ala Asn Ser Thr Ser Thr Glu Arg Lys Leu Pro Glu Pro Glu Ser Arg
 545 550 555
 ggc gtg gtc atc glg gct gtg att glg tgc atc ctg gtc ctg gcg gtg 1729
 Gly Val Val Ile Val Ala Val Ile Val Cys Ile Leu Val Leu Ala Val
 560 565 570
 ctg ggc gct gtc ctc tat ttc ctc tat aag aag ggc aag ctg ccg tgc 1777
 Leu Gly Ala Val Leu Tyr Phe Leu Tyr Lys Lys Gly Lys Leu Pro Cys
 575 580 585 590
 agg cgc tca ggg aag cag gag atc acg ctg ccc ccg tct cgt aag acc 1825
 Arg Arg Ser Gly Lys Gln Glu Ile Thr Leu Pro Pro Ser Arg Lys Thr
 595 600 605
 gaa ctt gta gtt gaa gtt aag tca gat aag ctc cca gaa gag atg ggc 1873
 Glu Leu Val Val Glu Val Lys Ser Asp Lys Leu Pro Glu Glu Met Gly
 610 615 620
 ctc ctg cag ggc agc agc ggt gac aag agg gct ccg gga gac cag gga 1921
 Leu Leu Gln Gly Ser Ser Gly Asp Lys Arg Ala Pro Gly Asp Gln Gly
 625 630 635
 gag aaa tac atc gat ctg agg cat tagccccgaa tcacttcagc tcccttcct 1975
 Glu Lys Tyr Ile Asp Leu Arg His

640

645

gccigggacca ttcccagctc ccigctcact ctctctcag ccaaagctca aagggactag 2035
 agagaagcct ccigctcccc tcgctgcac acccccttc agagggccac tgggttagga 2095
 cctgaggacc tcacttggcc ctgcaaggcc cgcttttcag ggaccagtcc accaccatct 2155
 cciccacgtt gaglgaagct catccaagc aaggagcccc agctctccga gcgggiagga 2215
 gaggttcttg cagaacgtgt ttttcttta cacacattat gctgtaaata cgctcgtcct 2275
 gccagcagct gagctgggta gcctctctga gctggtttcc tgcccaaaag gctggcattc 2335
 caccatccag gtcaccact gaagttagga cacaccggag ccaggcgccct gctcagtgtg 2395
 aagtgcgtcg ttacacccc ctccggagag caccacagca gcatccagaa gcagctgcag 2455
 tgcaagcttg catgcctgcg tgttctgca ccacctcct gctgcctct tcaaagtctc 2515
 ctgtgacatt tttcttttgg tcagaggcca ggaacttgtt catctcttaa agatcgtgc 2575
 cggggccagg tgtggctcac gcctglaac ccagcacitt gggaggccga ggcggcggat 2635
 cacaagctca gacgagacca tcctggctaa cacggtgaaa cctgtctct actaaaaata 2695
 caaaaaaaaa tttagctaggc gtagtgggtg gcacctatag tcccagctac tcggaaggct 2755
 gaagcaggag aatgggatga atccaggagg tggagcttgc agtgagccga gaccgtgcca 2815
 ctgcactcca gcctgggcaa cacagcgaga ctccgtctcg aggaaaaaaaaa aaatcgtgct 2875
 cgtagcagct ggctctgttt cgagtcaggt gaattagcct caatccccgt gttcacttgc 2935
 tcccatagcc ctcttgatgg atcacglaaa actgaaaggc agcggggagc agacaaagat 2995
 gaggtctaca ctgtccttca tggggattaa agctatggtt atattagcac caaacitcta 3055
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 ggcaaaacgg gcctggctag agcttcgggt gtgtgtgtgt gtcigtgtat gcatacatat 3175
 gtgtgtatat atggttttgt caggltgtta aatttgcaa ttgtttcctt tatatatgta 3235
 tgtatatata tatatgaaaa tatatatata tatgaaaaat aaagcttaat tgtcccag 3293

<210> 96

<211> 646

<212> PRT

<213> Homo sapiens

<400> 96

Met Gly Leu Pro Arg Leu Val Cys Ala Phe Leu Leu Ala Ala Cys Cys

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Cys Cys Pro Arg Val Ala Gly Val Pro Gly Glu Ala Glu Gln Pro Ala

20 25 30

Pro Glu Leu Val Glu Val Glu Val Gly Ser Thr Ala Leu Leu Lys Cys

35 40 45

Gly Leu Ser Gln Ser Gln Gly Asn Leu Ser His Val Asp Trp Phe Ser

50 55 60

Val His Lys Glu Lys Arg Thr Leu Ile Phe Arg Val Arg Gln Gly Gln

65 70 75 80

Gly Gln Ser Glu Pro Gly Glu Tyr Glu Gln Arg Leu Ser Leu Gln Asp

85 90 95

Arg Gly Ala Thr Leu Ala Leu Thr Gln Val Thr Pro Gln Asp Glu Arg

100 105 110

Ile Phe Leu Cys Gln Gly Lys Arg Pro Arg Ser Gln Glu Tyr Arg Ile

115 120 125

Gln Leu Arg Val Tyr Lys Ala Pro Glu Glu Pro Asn Ile Gln Val Asn

130 135 140

Pro Leu Gly Ile Pro Val Asn Ser Lys Glu Pro Glu Glu Val Ala Thr

145 150 155 160

Cys Val Gly Arg Asn Gly Tyr Pro Ile Pro Gln Val Ile Trp Tyr Lys

165 170 175

Asn Gly Arg Pro Leu Lys Glu Glu Lys Asn Arg Val His Ile Gln Ser

180 185 190

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Ser Gln Thr Val Glu Ser Ser Gly Leu Tyr Thr Leu Gln Ser Ile Leu
 195 200 205
 Lys Ala Gln Leu Val Lys Glu Asp Lys Asp Ala Gln Phe Tyr Cys Glu
 210 215 220
 Leu Asn Tyr Arg Leu Pro Ser Gly Asn His Met Lys Glu Ser Arg Glu
 225 230 235 240
 Val Thr Val Pro Val Phe Tyr Pro Thr Glu Lys Val Trp Leu Glu Val
 245 250 255
 Glu Pro Val Gly Met Leu Lys Glu Gly Asp Arg Val Glu Ile Arg Cys
 260 265 270
 Leu Ala Asp Gly Asn Pro Pro Pro His Phe Ser Ile Ser Lys Gln Asn
 275 280 285
 Pro Ser Thr Arg Glu Ala Glu Glu Glu Thr Thr Asn Asp Asn Gly Val
 290 295 300
 Leu Val Leu Glu Pro Ala Arg Lys Glu His Ser Gly Arg Tyr Glu Cys
 305 310 315 320
 Gln Ala Trp Asn Leu Asp Thr Met Ile Ser Leu Leu Ser Glu Pro Gln
 325 330 335
 Glu Leu Leu Val Asn Tyr Val Ser Asp Val Arg Val Ser Pro Ala Ala
 340 345 350
 Pro Glu Arg Gln Glu Gly Ser Ser Leu Thr Leu Thr Cys Glu Ala Glu
 355 360 365
 Ser Ser Gln Asp Leu Glu Phe Gln Trp Leu Arg Glu Glu Thr Asp Gln
 370 375 380
 Val Leu Glu Arg Gly Pro Val Leu Gln Leu His Asp Leu Lys Arg Glu
 385 390 395 400
 Ala Gly Gly Gly Tyr Arg Cys Val Ala Ser Val Pro Ser Ile Pro Gly

405 410 415
 Leu Asn Arg Thr Gln Leu Val Lys Leu Ala Ile Phe Gly Pro Pro Trp
 420 425 430
 Met Ala Phe Lys Glu Arg Lys Val Trp Val Lys Glu Asn Met Val Leu
 435 440 445
 Asn Leu Ser Cys Glu Ala Ser Gly His Pro Arg Pro Thr Ile Ser Trp
 450 455 460
 Asn Val Asn Gly Thr Ala Ser Glu Gln Asp Gln Asp Pro Gln Arg Val
 465 470 475 480
 Leu Ser Thr Leu Asn Val Leu Val Thr Pro Glu Leu Leu Glu Thr Gly
 485 490 495
 Val Glu Cys Thr Ala Ser Asn Asp Leu Gly Lys Asn Thr Ser Ile Leu
 500 505 510
 Phe Leu Glu Leu Val Asn Leu Thr Thr Leu Thr Pro Asp Ser Asn Thr
 515 520 525
 Thr Thr Gly Leu Ser Thr Ser Thr Ala Ser Pro His Thr Arg Ala Asn
 530 535 540
 Ser Thr Ser Thr Glu Arg Lys Leu Pro Glu Pro Glu Ser Arg Gly Val
 545 550 555 560
 Val Ile Val Ala Val Ile Val Cys Ile Leu Val Leu Ala Val Leu Gly
 565 570 575
 Ala Val Leu Tyr Phe Leu Tyr Lys Lys Gly Lys Leu Pro Cys Arg Arg
 580 585 590
 Ser Gly Lys Gln Glu Ile Thr Leu Pro Pro Ser Arg Lys Thr Glu Leu
 595 600 605
 Val Val Glu Val Lys Ser Asp Lys Leu Pro Glu Glu Met Gly Leu Leu

610 615 620
 Gln Gly Ser Ser Gly Asp Lys Arg Ala Pro Gly Asp Gln Gly Glu Lys
 625 630 635 640
 Tyr Ile Asp Leu Arg His
 645

<210> 97

<211> 1642

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (158).. (1279)

<400> 97

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 ggggaccagc agctgtcgcc gccgcctcga gggigaagag ggaacagaaa tctttgcccc 120
 ctgacttttg aaatctcggt taaccttcaa actggcg atg tca agg gtt cca agt 175

Met Ser Arg Val Pro Ser

1

5

cct cca cct ccg gca gaa atg tcg agt ggc ccc gta gct gag agt tgg 223

Pro Pro Pro Pro Ala Glu Met Ser Ser Gly Pro Val Ala Glu Ser Trp

10

15

20

tgc tac aca cag atc aag gta gtg aaa ttc tcc tac atg tgg acc atc 271

Cys Tyr Thr Gln Ile Lys Val Val Lys Phe Ser Tyr Met Trp Thr Ile

25

30

35

aat aac ttt agc ttt tgc cgg gag gaa atg ggt gaa gtc att aaa agt 319

Asn Asn Phe Ser Phe Cys Arg Glu Glu Met Gly Glu Val Ile Lys Ser

40	45	50	
tct aca ttt tca tca gga gca aat gat aaa ctg aaa tgg tgt ttg cga	367		
Ser Thr Phe Ser Ser Gly Ala Asn Asp Lys Leu Lys Trp Cys Leu Arg			
55	60	65	70
gta aac ccc aaa ggg tta gat gaa gaa agc aaa gat tac ctg tca ctt	415		
Val Asn Pro Lys Gly Leu Asp Glu Glu Ser Lys Asp Tyr Leu Ser Leu			
75	80	85	
tac ctg tta ctg gtc agc tgt cca aag agt gaa gtt cgg gca aaa ttc	463		
Tyr Leu Leu Leu Val Ser Cys Pro Lys Ser Glu Val Arg Ala Lys Phe			
90	95	100	
aaa ttc tcc atc ctg aat gcc aag gga gaa gaa acc aaa gct atg gag	511		
Lys Phe Ser Ile Leu Asn Ala Lys Gly Glu Glu Thr Lys Ala Met Glu			
105	110	115	
agt caa cgg gca tat agg ttt gtg caa ggc aaa gac tgg gga ttc aag	559		
Ser Gln Arg Ala Tyr Arg Phe Val Gln Gly Lys Asp Trp Gly Phe Lys			
120	125	130	
aaa ttc atc cgt aga gat ttt ctt ttg gat gag gcc aac ggg ctt ctc	607		
Lys Phe Ile Arg Arg Asp Phe Leu Leu Asp Glu Ala Asn Gly Leu Leu			
135	140	145	150
cct gat gac aag ctt acc ctc ttc tgc gag glg agt gtt gtg caa gat	655		
Pro Asp Asp Lys Leu Thr Leu Phe Cys Glu Val Ser Val Val Gln Asp			
155	160	165	
tct gtc aac att tct ggc cag aat acc atg aac atg gta aag gtt cct	703		
Ser Val Asn Ile Ser Gly Gln Asn Thr Met Asn Met Val Lys Val Pro			
170	175	180	
gag tgc cgg ctg gca gat gag tta gga gga ctg tgg gag aat tcc cgg	751		
Glu Cys Arg Leu Ala Asp Glu Leu Gly Gly Leu Trp Glu Asn Ser Arg			

185	190	195	
ttc aca gac tgc tgc ttg tgl gtt gcc ggc cag gaa ttc cag gct cac	799		
Phe Thr Asp Cys Cys Leu Cys Val Ala Gly Gln Glu Phe Gln Ala His			
200	205	210	
aag gct atc tta gca gct cgt tct ccg gtt ttt agt gcc atg ttt gaa	847		
Lys Ala Ile Leu Ala Ala Arg Ser Pro Val Phe Ser Ala Met Phe Glu			
215	220	225	230
cat gaa atg gag gag agc aaa aag aat cga gtt gaa atc aat gat gtg	895		
His Glu Met Glu Glu Ser Lys Lys Asn Arg Val Glu Ile Asn Asp Val			
235	240	245	
gag cct gaa gtt ttt aag gaa atg atg tgc ttc att tac acg ggg aag	943		
Glu Pro Glu Val Phe Lys Glu Met Met Cys Phe Ile Tyr Thr Gly Lys			
250	255	260	
gct cca aac ctc gac aaa atg gct gat gat ttg ctg gca gct gct gac	991		
Ala Pro Asn Leu Asp Lys Met Ala Asp Asp Leu Leu Ala Ala Ala Asp			
265	270	275	
aag tat gcc ctg gag cgc tta aag gtc atg tgt gag gat gcc ctc tgc	1039		
Lys Tyr Ala Leu Glu Arg Leu Lys Val Met Cys Glu Asp Ala Leu Cys			
280	285	290	
agt aac ctg tcc gtg gag aac gct gca gaa att ctc atc ctg gcc gac	1087		
Ser Asn Leu Ser Val Glu Asn Ala Ala Glu Ile Leu Ile Leu Ala Asp			
295	300	305	310
ctc cac agt gca gat cag ttg aaa act cag gca gtg gat ttc atc aac	1135		
Leu His Ser Ala Asp Gln Leu Lys Thr Gln Ala Val Asp Phe Ile Asn			
315	320	325	
tat cat gct tcg gat gtc ttg gag acc tct ggg tgg aag tca atg gtg	1183		

Tyr His Ala Ser Asp Val Leu Glu Thr Ser Gly Trp Lys Ser Met Val
 330 335 340
 gtg tca cat ccc cac ttg gtg gct gag gca tac cgc tct ctg gct tca 1231
 Val Ser His Pro His Leu Val Ala Glu Ala Tyr Arg Ser Leu Ala Ser
 345 350 355
 gca cag tgc cct ttt ctg gga ccc cca cgc aaa cgc ctg aag caa tcc 1279
 Ala Gln Cys Pro Phe Leu Gly Pro Pro Arg Lys Arg Leu Lys Gln Ser
 360 365 370
 taagatcctg ctgttgtaa gactccgttt aattccaga agcagcagcc actgttgctg 1339
 ccacigacca ccaggtagac agcgcaatct gaggagcttt tactctgttg tgagggaag 1399
 agactgcatt gggcccccag acitttaaaa cagcactaaa taacttgagg gaaacggggg 1459
 gagggaaaat gaaatgaaaa cctgttgct gcgicactgi gtccctttg gcctgtciga 1519
 gtttgatact gtggggattc agtttaggcg ctggcccgag gatacccag cggtggtact 1579
 tcggagacac ctgtctgcat ctgactgagc agaacaatc gtcaggigcc tggagcaaaa 1639
 agg 1642

<210> 98

<211> 374

<212> PRT

<213> Homo sapiens

<400> 98

Met Ser Arg Val Pro Ser Pro Pro Pro Pro Ala Glu Met Ser Ser Gly
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 Pro Val Ala Glu Ser Trp Cys Tyr Thr Gln Ile Lys Val Val Lys Phe
 20 25 30
 Ser Tyr Met Trp Thr Ile Asn Asn Phe Ser Phe Cys Arg Glu Glu Met
 35 40 45

Gly Glu Val Ile Lys Ser Ser Thr Phe Ser Ser Gly Ala Asn Asp Lys
 50 55 60
 Leu Lys Trp Cys Leu Arg Val Asn Pro Lys Gly Leu Asp Glu Glu Ser
 65 70 75 80
 Lys Asp Tyr Leu Ser Leu Tyr Leu Leu Leu Val Ser Cys Pro Lys Ser
 85 90 95
 Glu Val Arg Ala Lys Phe Lys Phe Ser Ile Leu Asn Ala Lys Gly Glu
 100 105 110
 Glu Thr Lys Ala Met Glu Ser Gln Arg Ala Tyr Arg Phe Val Gln Gly
 115 120 125
 Lys Asp Trp Gly Phe Lys Lys Phe Ile Arg Arg Asp Phe Leu Leu Asp
 130 135 140
 Glu Ala Asn Gly Leu Leu Pro Asp Asp Lys Leu Thr Leu Phe Cys Glu
 145 150 155 160
 Val Ser Val Val Gln Asp Ser Val Asn Ile Ser Gly Gln Asn Thr Met
 165 170 175
 Asn Met Val Lys Val Pro Glu Cys Arg Leu Ala Asp Glu Leu Gly Gly
 180 185 190
 Leu Trp Glu Asn Ser Arg Phe Thr Asp Cys Cys Leu Cys Val Ala Gly
 195 200 205
 Gln Glu Phe Gln Ala His Lys Ala Ile Leu Ala Ala Arg Ser Pro Val
 210 215 220
 Phe Ser Ala Met Phe Glu His Glu Met Glu Glu Ser Lys Lys Asn Arg
 225 230 235 240
 Val Glu Ile Asn Asp Val Glu Pro Glu Val Phe Lys Glu Met Met Cys
 245 250 255
 Phe Ile Tyr Thr Gly Lys Ala Pro Asn Leu Asp Lys Met Ala Asp Asp

260 265 270
 Leu Leu Ala Ala Ala Asp Lys Tyr Ala Leu Glu Arg Leu Lys Val Met
 275 280 285
 Cys Glu Asp Ala Leu Cys Ser Asn Leu Ser Val Glu Asn Ala Ala Glu
 290 295 300
 Ile Leu Ile Leu Ala Asp Leu His Ser Ala Asp Gln Leu Lys Thr Gln
 305 310 315 320
 Ala Val Asp Phe Ile Asn Tyr His Ala Ser Asp Val Leu Glu Thr Ser
 325 330 335
 Gly Trp Lys Ser Met Val Val Ser His Pro His Leu Val Ala Glu Ala
 340 345 350
 Tyr Arg Ser Leu Ala Ser Ala Gln Cys Pro Phe Leu Gly Pro Pro Arg
 355 360 365
 Lys Arg Leu Lys Gln Ser
 370

<210> 99

<211> 5722

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (112).. (3621)

<400> 99

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 cgccgcgctc cggtacacac aggatccctg ctgggcacca acagctccac c atg ggg 117

Met Gly

1

ctg gcc tgg gga cta ggc gtc ctg ttc ctg atg cat gtg tgt ggc acc 165
 Leu Ala Trp Gly Leu Gly Val Leu Phe Leu Met His Val Cys Gly Thr
 5 10 15
 aac cgc att cca gag tct ggc gga gac aac agc gtg ttt gac atc ttt 213
 Asn Arg Ile Pro Glu Ser Gly Gly Asp Asn Ser Val Phe Asp Ile Phe
 20 25 30
 gaa ctc acc ggg gcc gcc cgc aag ggg tct ggg cgc cga ctg gtg aag 261
 Glu Leu Thr Gly Ala Ala Arg Lys Gly Ser Gly Arg Arg Leu Val Lys
 35 40 45 50
 ggc ccc gac cct tcc agc cca gct ttc cgc atc gag gat gcc aac ctg 309
 Gly Pro Asp Pro Ser Ser Pro Ala Phe Arg Ile Glu Asp Ala Asn Leu
 55 60 65
 atc ccc cct gtg cct gat gac aag ttc caa gac ctg gtg gat gct gtg 357
 Ile Pro Pro Val Pro Asp Asp Lys Phe Gln Asp Leu Val Asp Ala Val
 70 75 80
 cgg gca gaa aag ggt ttc ctc ctt ctg gca tcc ctg agg cag atg aag 405
 Arg Ala Glu Lys Gly Phe Leu Leu Leu Ala Ser Leu Arg Gln Met Lys
 85 90 95
 aag acc cgg ggc acg ctg ctg gcc ctg gag cgg aaa gac cac tct ggc 453
 Lys Thr Arg Gly Thr Leu Leu Ala Leu Glu Arg Lys Asp His Ser Gly
 100 105 110
 cag gtc ttc agc gtg gtg tcc aat ggc aag gcg ggc acc ctg gac ctc 501
 Gln Val Phe Ser Val Val Ser Asn Gly Lys Ala Gly Thr Leu Asp Leu
 115 120 125 130
 agc ctg acc gtc caa gga aag cag cac gtg gtg tct gtg gaa gaa gct 549

Ser Leu Thr Val Gln Gly Lys Gln His Val Val Ser Val Glu Glu Ala
 135 140 145
 ctc ctg gca acc ggc cag tgg aag agc atc acc ctg ttt gtc cag gaa 597
 Leu Leu Ala Thr Gly Gln Trp Lys Ser Ile Thr Leu Phe Val Gln Glu
 150 155 160
 gac agg gcc cag ctg tac atc gac tgt gaa aag atg gag aat gct gag 645
 Asp Arg Ala Gln Leu Tyr Ile Asp Cys Glu Lys Met Glu Asn Ala Glu
 165 170 175
 ttg gac gtc ccc atc caa agc gtc ttc acc aga gac ctg gcc agc atc 693
 Leu Asp Val Pro Ile Gln Ser Val Phe Thr Arg Asp Leu Ala Ser Ile
 180 185 190
 gcc aga ctc cgc atc gca aag ggg ggc gtc aat gac aat ttc cag ggg 741
 Ala Arg Leu Arg Ile Ala Lys Gly Gly Val Asn Asp Asn Phe Gln Gly
 195 200 205 210
 gtg ctg cag aat gtg agg ttt gtc ttt gga acc aca cca gaa gac atc 789
 Val Leu Gln Asn Val Arg Phe Val Phe Gly Thr Thr Pro Glu Asp Ile
 215 220 225
 ctc agg aac aaa ggc tgc tcc agc tct acc agt gtc ctc ctc acc ctt 837
 Leu Arg Asn Lys Gly Cys Ser Ser Ser Thr Ser Val Leu Leu Thr Leu
 230 235 240
 gac aac aac gtg gtg aat ggt tcc agc cct gcc atc cgc act aac tac 885
 Asp Asn Asn Val Val Asn Gly Ser Ser Pro Ala Ile Arg Thr Asn Tyr
 245 250 255
 att ggc cac aag aca aag gac ttg caa gcc atc tgc ggc atc tcc tgt 933
 Ile Gly His Lys Thr Lys Asp Leu Gln Ala Ile Cys Gly Ile Ser Cys
 260 265 270
 gat gag ctg tcc agc atg gtc ctg gaa ctc agg ggc ctg cgc acc att 981

Asp Glu Leu Ser Ser Met Val Leu Glu Leu Arg Gly Leu Arg Thr Ile
 275 280 285 290
 gtg acc acg ctg cag gac agc atc cgc aaa gtg act gaa gag aac aaa 1029
 Val Thr Thr Leu Gln Asp Ser Ile Arg Lys Val Thr Glu Glu Asn Lys
 295 300 305
 gag ttg gcc aat gag ctg agg cgg cct ccc cta tgc tat cac aac gga 1077
 Glu Leu Ala Asn Glu Leu Arg Arg Pro Pro Leu Cys Tyr His Asn Gly
 310 315 320
 gtt cag tac aga aat aac gag gaa tgg act gtt gat agc tgc act gag 1125
 Val Gln Tyr Arg Asn Asn Glu Glu Trp Thr Val Asp Ser Cys Thr Glu
 325 330 335
 tgt cac tgt cag aac tca gtt acc atc tgc aaa aag gtg tcc tgc ccc 1173
 Cys His Cys Gln Asn Ser Val Thr Ile Cys Lys Lys Val Ser Cys Pro
 340 345 350
 atc atg ccc tgc tcc aat gcc aca gtt cct gat gga gaa tgc tgt cct 1221
 Ile Met Pro Cys Ser Asn Ala Thr Val Pro Asp Gly Glu Cys Cys Pro
 355 360 365 370
 cgc tgt tgg ccc agc gac tct gcg gac gat ggc tgg tct cca tgg tcc 1269
 Arg Cys Trp Pro Ser Asp Ser Ala Asp Asp Gly Trp Ser Pro Trp Ser
 375 380 385
 gag tgg acc tcc tgt tct acg agc tgt ggc aat gga att cag cag cgc 1317
 Glu Trp Thr Ser Cys Ser Thr Ser Cys Gly Asn Gly Ile Gln Gln Arg
 390 395 400
 ggc cgc tcc tgc gat agc ctc aac aac cga tgt gag ggc tcc tgc gtc 1365
 Gly Arg Ser Cys Asp Ser Leu Asn Asn Arg Cys Glu Gly Ser Ser Val
 405 410 415

cag aca cgg acc tgc cac att cag gag tgt gac aaa aga ttt aaa cag 1413
 Gln Thr Arg Thr Cys His Ile Gln Glu Cys Asp Lys Arg Phe Lys Gln
 420 425 430
 gat ggt ggc tgg agc cac tgg tcc ccg tgg tca tct tgt tct gtg aca 1461
 Asp Gly Gly Trp Ser His Trp Ser Pro Trp Ser Ser Cys Ser Val Thr
 435 440 445 450
 tgt ggt gat ggt gtg atc aca agg atc cgg ctc tgc aac tct ccc agc 1509
 Cys Gly Asp Gly Val Ile Thr Arg Ile Arg Leu Cys Asn Ser Pro Ser
 455 460 465
 ccc cag atg aat ggg aaa ccc tgt gaa ggc gaa gcg cgg gag acc aaa 1557
 Pro Gln Met Asn Gly Lys Pro Cys Glu Gly Glu Ala Arg Glu Thr Lys
 470 475 480
 gcc tgc aag aaa gac gcc tgc ccc atc aat gga ggc tgg ggt cct tgg 1605
 Ala Cys Lys Lys Asp Ala Cys Pro Ile Asn Gly Gly Trp Gly Pro Trp
 485 490 495
 tca cca tgg gac atc tgt tct gtc acc tgt gga gga ggg gta cag aaa 1653
 Ser Pro Trp Asp Ile Cys Ser Val Thr Cys Gly Gly Gly Val Gln Lys
 500 505 510
 cgt agt cgt ctc tgc aac aac ccc gca ccc cag ttt gga ggc aag gac 1701
 Arg Ser Arg Leu Cys Asn Asn Pro Ala Pro Gln Phe Gly Gly Lys Asp
 515 520 525 530
 tgc gtt ggt gat gta aca gaa aac cag atc tgc aac aag cag gac tgt 1749
 Cys Val Gly Asp Val Thr Glu Asn Gln Ile Cys Asn Lys Gln Asp Cys
 535 540 545
 cca att gat gga tgc ctg tcc aat ccc tgc ttt gcc ggc gtg aag tgt 1797
 Pro Ile Asp Gly Cys Leu Ser Asn Pro Cys Phe Ala Gly Val Lys Cys
 550 555 560

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act agc tac cct gat ggc agc tgg aaa tgt ggt gct tgt ccc cct ggt 1845
 Thr Ser Tyr Pro Asp Gly Ser Trp Lys Cys Gly Ala Cys Pro Pro Gly
 565 570 575
 tac agt gga aat ggc atc cag tgc aca gat gtt gat gag tgc aaa gaa 1893
 Tyr Ser Gly Asn Gly Ile Gln Cys Thr Asp Val Asp Glu Cys Lys Glu
 580 585 590
 gtg cct gat gcc tgc ttc aac cac aat gga gag cac cgg tgt gag aac 1941
 Val Pro Asp Ala Cys Phe Asn His Asn Gly Glu His Arg Cys Glu Asn
 595 600 605 610
 acg gac ccc ggc tac aac tgc ctg ccc tgc ccc cca cgc ttc acc ggc 1989
 Thr Asp Pro Gly Tyr Asn Cys Leu Pro Cys Pro Pro Arg Phe Thr Gly
 615 620 625
 tca cag ccc ttc ggc cag ggt gtc gaa cat gcc acg gcc aac aaa cag 2037
 Ser Gln Pro Phe Gly Gln Gly Val Glu His Ala Thr Ala Asn Lys Gln
 630 635 640
 gtg tgc aag ccc cgt aac ccc tgc acg gat ggg acc cac gac tgc aac 2085
 Val Cys Lys Pro Arg Asn Pro Cys Thr Asp Gly Thr His Asp Cys Asn
 645 650 655
 aag aac gcc aag tgc aac tac ctg ggc cac tat agc gac ccc atg tac 2133
 Lys Asn Ala Lys Cys Asn Tyr Leu Gly His Tyr Ser Asp Pro Met Tyr
 660 665 670
 cgc tgc gag tgc aag cct ggc tac gct ggc aat ggc atc atc tgc ggg 2181
 Arg Cys Glu Cys Lys Pro Gly Tyr Ala Gly Asn Gly Ile Ile Cys Gly
 675 680 685 690
 gag gac aca gac ctg gat ggc tgg ccc aat gag aac ctg gtg tgc gtg 2229
 Glu Asp Thr Asp Leu Asp Gly Trp Pro Asn Glu Asn Leu Val Cys Val

695	700	705	
gcc aat gcg act tac cac tgc aaa aag gat aat tgc ccc aac ctt ccc	2277		
Ala Asn Ala Thr Tyr His Cys Lys Lys Asp Asn Cys Pro Asn Leu Pro			
710	715	720	
aac tca ggg cag gaa gac tat gac aag gat gga att ggt gat gcc tgt	2325		
Asn Ser Gly Gln Glu Asp Tyr Asp Lys Asp Gly Ile Gly Asp Ala Cys			
725	730	735	
gat gat gac gat gac aat gat aaa att cca gat gac agg gac aac tgt	2373		
Asp Asp Asp Asp Asp Asn Asp Lys Ile Pro Asp Asp Arg Asp Asn Cys			
740	745	750	
cca ttc cat tac aac cca gct cag tat gac tat gac aga gat gat gtg	2421		
Pro Phe His Tyr Asn Pro Ala Gln Tyr Asp Tyr Asp Arg Asp Asp Val			
755	760	765	770
gga gac cgc tgt gac aac tgt ccc tac aac cac aac cca gat cag gca	2469		
Gly Asp Arg Cys Asp Asn Cys Pro Tyr Asn His Asn Pro Asp Gln Ala			
775	780	785	
gac aca gac aac aat ggg gaa gga gac gcc tgt gct gca gac att gat	2517		
Asp Thr Asp Asn Asn Gly Glu Gly Asp Ala Cys Ala Ala Asp Ile Asp			
790	795	800	
gga gac ggt atc ctc aat gaa cgg gac aac tgc cag tac gtc tac aat	2565		
Gly Asp Gly Ile Leu Asn Glu Arg Asp Asn Cys Gln Tyr Val Tyr Asn			
805	810	815	
gtg gac cag aga gac act gat atg gat ggg gtt gga gat cag tgt gac	2613		
Val Asp Gln Arg Asp Thr Asp Met Asp Gly Val Gly Asp Gln Cys Asp			
820	825	830	
aat tgc ccc ttg gaa cac aat ccg gat cag ctg gac tct gac tca gac	2661		
Asn Cys Pro Leu Glu His Asn Pro Asp Gln Leu Asp Ser Asp Ser Asp			

835	840	845	850	
cgc att gga gat acc tgt gac aac aat cag gai att gat gaa gat ggc	2709			
Arg Ile Gly Asp Thr Cys Asp Asn Asn Gln Asp Ile Asp Glu Asp Gly				
855	860	865		
cac cag aac aat ctg gac aac tgt ccc tat gtg ccc aat gcc aac cag	2757			
His Gln Asn Asn Leu Asp Asn Cys Pro Tyr Val Pro Asn Ala Asn Gln				
870	875	880		
gct gac cat gac aaa gat ggc aag gga gat gcc tgt gac cac gat gat	2805			
Ala Asp His Asp Lys Asp Gly Lys Gly Asp Ala Cys Asp His Asp Asp				
885	890	895		
gac aac gat ggc att cct gat gac aag gac aac tgc aga ctc gtg ccc	2853			
Asp Asn Asp Gly Ile Pro Asp Asp Lys Asp Asn Cys Arg Leu Val Pro				
900	905	910		
aat ccc gac cag aag gac tct gac ggc gat ggt cga ggt gat gcc tgc	2901			
Asn Pro Asp Gln Lys Asp Ser Asp Gly Asp Gly Arg Gly Asp Ala Cys				
915	920	925	930	
aaa gat gat ttt gac cat gac agt gtg cca gac atc gat gac atc tgt	2949			
Lys Asp Asp Phe Asp His Asp Ser Val Pro Asp Ile Asp Asp Ile Cys				
935	940	945		
cct gag aat gtt gac atc agt gag acc gat ttc cgc cga ttc cag atg	2997			
Pro Glu Asn Val Asp Ile Ser Glu Thr Asp Phe Arg Arg Phe Gln Met				
950	955	960		
att cct ctg gac ccc aaa ggg aca tcc caa aat gac cct aac tgg gtt	3045			
Ile Pro Leu Asp Pro Lys Gly Thr Ser Gln Asn Asp Pro Asn Trp Val				
965	970	975		
gta cgc cat cag ggt aaa gaa ctc gtc cag act gtc aac tgt gat cct	3093			

Val Arg His Gln Gly Lys Glu Leu Val Gln Thr Val Asn Cys Asp Pro
 980 985 990
 gga ctc gct gta ggt tat gat gag ttt aat gct gtg gac ttc agt ggc 3141
 Gly Leu Ala Val Gly Tyr Asp Glu Phe Asn Ala Val Asp Phe Ser Gly
 995 1000 1005 1010
 acc ttc ttc atc aac acc gaa agg gac gat gac tat gct gga ttt gtc 3189
 Thr Phe Phe Ile Asn Thr Glu Arg Asp Asp Asp Tyr Ala Gly Phe Val
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 Phe Gly Tyr Gln Ser Ser Ser Arg Phe Tyr Val Val Met Trp Lys Gln
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 Val Thr Gln Ser Tyr Trp Asp Thr Asn Pro Thr Arg Ala Gln Gly Tyr
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 tcg ggc ctt tct gtg aaa gtt gta aac tcc acc aca ggc cct ggc gag 3333
 Ser Gly Leu Ser Val Lys Val Val Asn Ser Thr Thr Gly Pro Gly Glu
 1060 1065 1070
 cac ctg cgg aac gcc ctg tgg cac aca gga aac acc cct ggc cag gtg 3381
 His Leu Arg Asn Ala Leu Trp His Thr Gly Asn Thr Pro Gly Gln Val
 1075 1080 1085 1090
 cgc acc ctg tgg cat gac cct cgt cac ata ggc tgg aaa gat ttc acc 3429
 Arg Thr Leu Trp His Asp Pro Arg His Ile Gly Trp Lys Asp Phe Thr
 1095 1100 1105
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 Ala Tyr Arg Trp Arg Leu Ser His Arg Pro Lys Thr Gly Phe Ile Arg
 1110 1115 1120
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Val Val Met Tyr Glu Gly Lys Lys Ile Met Ala Asp Ser Gly Pro Ile

1125

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1135

tat gat aaa acc tat gct ggt ggt aga cta ggg ttg ttt gtc ttc tct 3573

Tyr Asp Lys Thr Tyr Ala Gly Gly Arg Leu Gly Leu Phe Val Phe Ser

1140

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caa gaa atg gtg ttc ttc tct gac ctg aaa tac gaa tgt aga gat ccc 3621

Gln Glu Met Val Phe Phe Ser Asp Leu Lys Tyr Glu Cys Arg Asp Pro

1155

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1165

1170

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<210> 100

<211> 1170

<212> PRT

<213> Homo sapiens

<400> 100

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WO 01/25427

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 Ile Phe Glu Leu Thr Gly Ala Ala Arg Lys Gly Ser Gly Arg Arg Leu
 35 40 45
 Val Lys Gly Pro Asp Pro Ser Ser Pro Ala Phe Arg Ile Glu Asp Ala
 50 55 60
 Asn Leu Ile Pro Pro Val Pro Asp Asp Lys Phe Gln Asp Leu Val Asp
 65 70 75 80
 Ala Val Arg Ala Glu Lys Gly Phe Leu Leu Leu Ala Ser Leu Arg Gln
 85 90 95
 Met Lys Lys Thr Arg Gly Thr Leu Leu Ala Leu Glu Arg Lys Asp His
 100 105 110
 Ser Gly Gln Val Phe Ser Val Val Ser Asn Gly Lys Ala Gly Thr Leu
 115 120 125
 Asp Leu Ser Leu Thr Val Gln Gly Lys Gln His Val Val Ser Val Glu
 130 135 140
 Glu Ala Leu Leu Ala Thr Gly Gln Trp Lys Ser Ile Thr Leu Phe Val
 145 150 155 160
 Gln Glu Asp Arg Ala Gln Leu Tyr Ile Asp Cys Glu Lys Met Glu Asn
 165 170 175
 Ala Glu Leu Asp Val Pro Ile Gln Ser Val Phe Thr Arg Asp Leu Ala
 180 185 190
 Ser Ile Ala Arg Leu Arg Ile Ala Lys Gly Gly Val Asn Asp Asn Phe
 195 200 205
 Gln Gly Val Leu Gln Asn Val Arg Phe Val Phe Gly Thr Thr Pro Glu
 210 215 220
 Asp Ile Leu Arg Asn Lys Gly Cys Ser Ser Ser Thr Ser Val Leu Leu
 225 230 235 240

WO 01/25427

Thr Leu Asp Asn Asn Val Val Asn Gly Ser Ser Pro Ala Ile Arg Thr
 245 250 255
 Asn Tyr Ile Gly His Lys Thr Lys Asp Leu Gln Ala Ile Cys Gly Ile
 260 265 270
 Ser Cys Asp Glu Leu Ser Ser Met Val Leu Glu Leu Arg Gly Leu Arg
 275 280 285
 Thr Ile Val Thr Thr Leu Gln Asp Ser Ile Arg Lys Val Thr Glu Glu
 290 295 300
 Asn Lys Glu Leu Ala Asn Glu Leu Arg Arg Pro Pro Leu Cys Tyr His
 305 310 315 320
 Asn Gly Val Gln Tyr Arg Asn Asn Glu Glu Trp Thr Val Asp Ser Cys
 325 330 335
 Thr Glu Cys His Cys Gln Asn Ser Val Thr Ile Cys Lys Lys Val Ser
 340 345 350
 Cys Pro Ile Met Pro Cys Ser Asn Ala Thr Val Pro Asp Gly Glu Cys
 355 360 365
 Cys Pro Arg Cys Trp Pro Ser Asp Ser Ala Asp Asp Gly Trp Ser Pro
 370 375 380
 Trp Ser Glu Trp Thr Ser Cys Ser Thr Ser Cys Gly Asn Gly Ile Gln
 385 390 395 400
 Gln Arg Gly Arg Ser Cys Asp Ser Leu Asn Asn Arg Cys Glu Gly Ser
 405 410 415
 Ser Val Gln Thr Arg Thr Cys His Ile Gln Glu Cys Asp Lys Arg Phe
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 Lys Gln Asp Gly Gly Trp Ser His Trp Ser Pro Trp Ser Ser Cys Ser
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Val Thr Cys Gly Asp Gly Val Ile Thr Arg Ile Arg Leu Cys Asn Ser
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Pro Ser Pro Gln Met Asn Gly Lys Pro Cys Glu Gly Glu Ala Arg Glu
465 470 475 480
Thr Lys Ala Cys Lys Lys Asp Ala Cys Pro Ile Asn Gly Gly Trp Gly
485 490 495
Pro Trp Ser Pro Trp Asp Ile Cys Ser Val Thr Cys Gly Gly Gly Val
500 505 510
Gln Lys Arg Ser Arg Leu Cys Asn Asn Pro Ala Pro Gln Phe Gly Gly
515 520 525
Lys Asp Cys Val Gly Asp Val Thr Glu Asn Gln Ile Cys Asn Lys Gln
530 535 540
Asp Cys Pro Ile Asp Gly Cys Leu Ser Asn Pro Cys Phe Ala Gly Val
545 550 555 560
Lys Cys Thr Ser Tyr Pro Asp Gly Ser Trp Lys Cys Gly Ala Cys Pro
565 570 575
Pro Gly Tyr Ser Gly Asn Gly Ile Gln Cys Thr Asp Val Asp Glu Cys
580 585 590
Lys Glu Val Pro Asp Ala Cys Phe Asn His Asn Gly Glu His Arg Cys
595 600 605
Glu Asn Thr Asp Pro Gly Tyr Asn Cys Leu Pro Cys Pro Pro Arg Phe
610 615 620
Thr Gly Ser Gln Pro Phe Gly Gln Gly Val Glu His Ala Thr Ala Asn
625 630 635 640
Lys Gln Val Cys Lys Pro Arg Asn Pro Cys Thr Asp Gly Thr His Asp
645 650 655
Cys Asn Lys Asn Ala Lys Cys Asn Tyr Leu Gly His Tyr Ser Asp Pro

WO 01/25427

660	665	670	
Met Tyr Arg Cys Glu Cys Lys Pro Gly Tyr Ala Gly Asn Gly Ile Ile			
675	680	685	
Cys Gly Glu Asp Thr Asp Leu Asp Gly Trp Pro Asn Glu Asn Leu Val			
690	695	700	
Cys Val Ala Asn Ala Thr Tyr His Cys Lys Lys Asp Asn Cys Pro Asn			
705	710	715	720
Leu Pro Asn Ser Gly Gln Glu Asp Tyr Asp Lys Asp Gly Ile Gly Asp			
725	730	735	
Ala Cys Asp Asp Asp Asp Asp Asn Asp Lys Ile Pro Asp Asp Arg Asp			
740	745	750	
Asn Cys Pro Phe His Tyr Asn Pro Ala Gln Tyr Asp Tyr Asp Arg Asp			
755	760	765	
Asp Val Gly Asp Arg Cys Asp Asn Cys Pro Tyr Asn His Asn Pro Asp			
770	775	780	
Gln Ala Asp Thr Asp Asn Asn Gly Glu Gly Asp Ala Cys Ala Ala Asp			
785	790	795	800
Ile Asp Gly Asp Gly Ile Leu Asn Glu Arg Asp Asn Cys Gln Tyr Val			
805	810	815	
Tyr Asn Val Asp Gln Arg Asp Thr Asp Met Asp Gly Val Gly Asp Gln			
820	825	830	
Cys Asp Asn Cys Pro Leu Glu His Asn Pro Asp Gln Leu Asp Ser Asp			
835	840	845	
Ser Asp Arg Ile Gly Asp Thr Cys Asp Asn Asn Gln Asp Ile Asp Glu			
850	855	860	
Asp Gly His Gln Asn Asn Leu Asp Asn Cys Pro Tyr Val Pro Asn Ala			

WO 01/25427

865 870 875 880
 Asn Gln Ala Asp His Asp Lys Asp Gly Lys Gly Asp Ala Cys Asp His
 885 890 895
 Asp Asp Asp Asn Asp Gly Ile Pro Asp Asp Lys Asp Asn Cys Arg Leu
 900 905 910
 Val Pro Asn Pro Asp Gln Lys Asp Ser Asp Gly Asp Gly Arg Gly Asp
 915 920 925
 Ala Cys Lys Asp Asp Phe Asp His Asp Ser Val Pro Asp Ile Asp Asp
 930 935 940
 Ile Cys Pro Glu Asn Val Asp Ile Ser Glu Thr Asp Phe Arg Arg Phe
 945 950 955 960
 Gln Met Ile Pro Leu Asp Pro Lys Gly Thr Ser Gln Asn Asp Pro Asn
 965 970 975
 Trp Val Val Arg His Gln Gly Lys Glu Leu Val Gln Thr Val Asn Cys
 980 985 990
 Asp Pro Gly Leu Ala Val Gly Tyr Asp Glu Phe Asn Ala Val Asp Phe
 995 1000 1005
 Ser Gly Thr Phe Phe Ile Asn Thr Glu Arg Asp Asp Asp Tyr Ala Gly
 1010 1015 1020
 Phe Val Phe Gly Tyr Gln Ser Ser Ser Arg Phe Tyr Val Val Met Trp
 1025 1030 1035 1040
 Lys Gln Val Thr Gln Ser Tyr Trp Asp Thr Asn Pro Thr Arg Ala Gln
 1045 1050 1055
 Gly Tyr Ser Gly Leu Ser Val Lys Val Val Asn Ser Thr Thr Gly Pro
 1060 1065 1070
 Gly Glu His Leu Arg Asn Ala Leu Trp His Thr Gly Asn Thr Pro Gly
 1075 1080 1085

Gln Val Arg Thr Leu Trp His Asp Pro Arg His Ile Gly Trp Lys Asp

1090

1095

1100

Phe Thr Ala Tyr Arg Trp Arg Leu Ser His Arg Pro Lys Thr Gly Phe

1105

1110

1115

1120

Ile Arg Val Val Met Tyr Glu Gly Lys Lys Ile Met Ala Asp Ser Gly

1125

1130

1135

Pro Ile Tyr Asp Lys Thr Tyr Ala Gly Gly Arg Leu Gly Leu Phe Val

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Phe Ser Gln Glu Met Val Phe Phe Ser Asp Leu Lys Tyr Glu Cys Arg

1155

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Asp Pro

1170

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<211> 838

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (35).. (568)

<400> 101

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Met Ser Gly Gly Lys Tyr Val

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gac tcg gag gga cat ctc tac acc gtt ccc atc cgg gaa cag ggc aac 103

Asp Ser Glu Gly His Leu Tyr Thr Val Pro Ile Arg Glu Gln Gly Asn

10

15

20

atc tac aag ccc aac aac aag gcc atg gca gac gag ctg agc gag aag 151
Ile Tyr Lys Pro Asn Asn Lys Ala Met Ala Asp Glu Leu Ser Glu Lys
25 30 35
caa gtg tac gac gcg cac acc aag gag atc gac ctg gtc aac cgc gac 199
Gln Val Tyr Asp Ala His Thr Lys Glu Ile Asp Leu Val Asn Arg Asp
40 45 50 55
cct aaa cac ctc aac gat gac gtg gtc aag att gac ttt gaa gat gtg 247
Pro Lys His Leu Asn Asp Asp Val Val Lys Ile Asp Phe Glu Asp Val
60 65 70
att gca gaa cca gaa ggg aca cac agt ttt cac ggc att tgg aag gcc 295
Ile Ala Glu Pro Glu Gly Thr His Ser Phe His Gly Ile Trp Lys Ala
75 80 85
agc ttc acc acc ttc act gtg acg aaa tac tgg ttt tac cgc ttg ctg 343
Ser Phe Thr Thr Phe Thr Val Thr Lys Tyr Trp Phe Tyr Arg Leu Leu
90 95 100
tct gcc ctc ttt ggc atc ccg atg gca ctc atc tgg ggc att tac ttc 391
Ser Ala Leu Phe Gly Ile Pro Met Ala Leu Ile Trp Gly Ile Tyr Phe
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gcc att ctc tct ttc ctg cac atc tgg gca gtt gta cca tgc att aag 439
Ala Ile Leu Ser Phe Leu His Ile Trp Ala Val Val Pro Cys Ile Lys
120 125 130 135
agc ttc ctg att gag att cag tgc acc agc cgt gtc tat tcc atc tac 487
Ser Phe Leu Ile Glu Ile Gln Cys Thr Ser Arg Val Tyr Ser Ile Tyr
140 145 150
gtc cac acc gtc tgt gac cca ctc ttt gaa gct gtt ggg aaa ata ttc 535
Val His Thr Val Cys Asp Pro Leu Phe Glu Ala Val Gly Lys Ile Phe

155 160 165
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<211> 178

<212> PRT

<213> Homo sapiens

<400> 102

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 Ala Asp Glu Leu Ser Glu Lys Gln Val Tyr Asp Ala His Thr Lys Glu
 35 40 45
 Ile Asp Leu Val Asn Arg Asp Pro Lys His Leu Asn Asp Asp Val Val
 50 55 60
 Lys Ile Asp Phe Glu Asp Val Ile Ala Glu Pro Glu Gly Thr His Ser
 65 70 75 80
 Phe His Gly Ile Trp Lys Ala Ser Phe Thr Thr Phe Thr Val Thr Lys
 85 90 95

Tyr Trp Phe Tyr Arg Leu Leu Ser Ala Leu Phe Gly Ile Pro Met Ala

100

105

110

Leu Ile Trp Gly Ile Tyr Phe Ala Ile Leu Ser Phe Leu His Ile Trp

115

120

125

Ala Val Val Pro Cys Ile Lys Ser Phe Leu Ile Glu Ile Gln Cys Thr

130

135

140

Ser Arg Val Tyr Ser Ile Tyr Val His Thr Val Cys Asp Pro Leu Phe

145

150

155

160

Glu Ala Val Gly Lys Ile Phe Ser Asn Val Arg Ile Asn Leu Gln Lys

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170

175

Glu Ile

<210> 103

<211> 2269

<212> DNA

<213> Homo sapiens

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<221> CDS

<222> (1).. (444)

<400> 103

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Leu Phe Leu Thr Ile Pro Phe Ala Phe Phe Leu Pro Glu Leu Ile Phe

20

25

30

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 Ser Leu Met Phe Leu Leu Ser Tyr Leu Phe Gly Phe Tyr Lys Arg Phe
 65 70 75 80
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 Glu Ser Trp Arg Val Leu Asp Ser Leu Tyr His Gly Thr Thr Gly Ile
 85 90 95
 ctg tac atg agc gct gcc gtc cta caa gta cat gcc acg att gtt tct 336
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 Ile Tyr Tyr His
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<211> 148

<212> PRT

<213> Homo sapiens

<400> 104

Pro Pro Ala Thr Ser Tyr Ala Pro Ser Asp Val Pro Ser Gly Val Ala

1 5 10 15

Leu Phe Leu Thr Ile Pro Phe Ala Phe Phe Leu Pro Glu Leu Ile Phe

20 25 30

Gly Phe Leu Val Trp Thr Met Val Ala Ala Thr His Ile Val Tyr Pro

35 40 45

Leu Leu Gln Gly Trp Val Met Tyr Val Ser Leu Thr Ser Phe Leu Ile

50 55 60

Ser Leu Met Phe Leu Leu Ser Tyr Leu Phe Gly Phe Tyr Lys Arg Phe

65 70 75 80

Glu Ser Trp Arg Val Leu Asp Ser Leu Tyr His Gly Thr Thr Gly Ile

85 90 95

Leu Tyr Met Ser Ala Ala Val Leu Gln Val His Ala Thr Ile Val Ser

100 105 110

Glu Lys Leu Leu Asp Pro Arg Ile Tyr Tyr Ile Asn Ser Ala Ala Ser

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Phe Phe Ala Phe Ile Ala Thr Leu Leu Tyr Ile Leu His Ala Phe Ser

130 135 140

Ile Tyr Tyr His

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<210> 105

<211> 2899

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (91).. (2196)

<400> 105

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 gggcctcggc tacttggact gcggcggaat atg gcg gct ccg atg act ccc gcg 114

Met Ala Ala Pro Met Thr Pro Ala

1

5

gct cgg ccc gag gac tac gag gcg gcg ctg aat gcc gcc ctg gct gac 162
 Ala Arg Pro Glu Asp Tyr Glu Ala Ala Leu Asn Ala Ala Leu Ala Asp

10

15

20

gtg ccc gaa ctg gcc aga ctg ctg gag atc gac ccg tac ttg aag ccc 210
 Val Pro Glu Leu Ala Arg Leu Leu Glu Ile Asp Pro Tyr Leu Lys Pro

25

30

35

40

tac gcc gtg gac ttc cag cgc agg tat aag cag ttt agc caa att ttg 258
 Tyr Ala Val Asp Phe Gln Arg Arg Tyr Lys Gln Phe Ser Gln Ile Leu

45

50

55

aag aac att gga gaa aat gaa ggt ggt att gat aag ttt tcc aga ggc 306
 Lys Asn Ile Gly Glu Asn Glu Gly Gly Ile Asp Lys Phe Ser Arg Gly

60

65

70

tat gaa tca ttt ggc gtc cac aga tgt gct gat ggt ggt tta tac tcc 354
 Tyr Glu Ser Phe Gly Val His Arg Cys Ala Asp Gly Gly Leu Tyr Ser

75

80

85

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aaa gaa tgg gcc ccg gga gca gaa gga gtt ttt ctt act gga gat ttt 402
Lys Glu Trp Ala Pro Gly Ala Glu Gly Val Phe Leu Thr Gly Asp Phe
    90                95                100

aat ggt tgg aat cca ttt tcg tac cca tac aaa aaa ctg gat tat gga 450
Asn Gly Trp Asn Pro Phe Ser Tyr Pro Tyr Lys Lys Leu Asp Tyr Gly
105                110                115                120

aaa tgg gag ctg tat atc cca cca aag cag aat aaa tct gta ctc gtg 498
Lys Trp Glu Leu Tyr Ile Pro Pro Lys Gln Asn Lys Ser Val Leu Val
    125                130                135

cct cat gga tcc aaa tta aag gta gtt att act agt aaa agc gga gag 546
Pro His Gly Ser Lys Leu Lys Val Val Ile Thr Ser Lys Ser Gly Glu
    140                145                150

atc ttg tat cgt att tca ccg tgg gca aag tat gtg gtt cgt gaa ggt 594
Ile Leu Tyr Arg Ile Ser Pro Trp Ala Lys Tyr Val Val Arg Glu Gly
    155                160                165

gat aat gtg aat tat gat tgg ata cac tgg gat cca gaa cac tca tat 642
Asp Asn Val Asn Tyr Asp Trp Ile His Trp Asp Pro Glu His Ser Tyr
    170                175                180

gag ttt aag cat tcc aga cca aag aag cca cgg agt cta aga att tat 690
Glu Phe Lys His Ser Arg Pro Lys Lys Pro Arg Ser Leu Arg Ile Tyr
185                190                195                200

gaa tct cat gtg gga att tct tcc cat gaa gga aaa gta gct tct tat 738
Glu Ser His Val Gly Ile Ser Ser His Glu Gly Lys Val Ala Ser Tyr
    205                210                215

aaa cat ttt aca tgc aat gta cta cca aga atc aaa ggc ctt gga tac 786
Lys His Phe Thr Cys Asn Val Leu Pro Arg Ile Lys Gly Leu Gly Tyr
    220                225                230

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aac tgc att cag ttg atg gca atc atg gag cat gct tac tat gcc agc 834
 Asn Cys Ile Gln Leu Met Ala Ile Met Glu His Ala Tyr Tyr Ala Ser
 235 240 245
 ttt ggt tac caa atc aca agc ttc ttt gca gct tcc agc cgt tat gga 882
 Phe Gly Tyr Gln Ile Thr Ser Phe Phe Ala Ala Ser Ser Arg Tyr Gly
 250 255 260
 aca cct gaa gag cta caa gaa ctg gta gac aca gct cat tcc atg ggt 930
 Thr Pro Glu Glu Leu Gln Glu Leu Val Asp Thr Ala His Ser Met Gly
 265 270 275 280
 atc ata gtc ctc tta gat gtg gla cac agc cat gct tca aaa aat tca 978
 Ile Ile Val Leu Leu Asp Val Val His Ser His Ala Ser Lys Asn Ser
 285 290 295
 gca gat gga ttg aat atg ttt gat ggg aca gat tcc tgt tat ttt cat 1026
 Ala Asp Gly Leu Asn Met Phe Asp Gly Thr Asp Ser Cys Tyr Phe His
 300 305 310
 tct gga cct aga ggg act cat gat ctt tgg gat agc aga ttg ttt gcc 1074
 Ser Gly Pro Arg Gly Thr His Asp Leu Trp Asp Ser Arg Leu Phe Ala
 315 320 325
 tac tcc agc tgg gaa gtt tta aga ttc ctt ctg tca aac ata aga tgg 1122
 Tyr Ser Ser Trp Glu Val Leu Arg Phe Leu Leu Ser Asn Ile Arg Trp
 330 335 340
 tgg ttg gaa gaa tat cgc ttt gat gga ttt cgt ttt gat ggt gtt acg 1170
 Trp Leu Glu Glu Tyr Arg Phe Asp Gly Phe Arg Phe Asp Gly Val Thr
 345 350 355 360
 tcc atg ctt tat cat cac cat gga gtg ggt caa ggt ttc tca ggt gat 1218
 Ser Met Leu Tyr His His His Gly Val Gly Gln Gly Phe Ser Gly Asp

365	370	375	
tac agt gaa tat ttc gga cta caa gla gat gaa gat gcc ttg act tac	1266		
Tyr Ser Glu Tyr Phe Gly Leu Gln Val Asp Glu Asp Ala Leu Thr Tyr			
380	385	390	
ctc atg ttg gca aat cat ttg gtt cac acg ctg tgt ccc gat tct ata	1314		
Leu Met Leu Ala Asn His Leu Val His Thr Leu Cys Pro Asp Ser Ile			
395	400	405	
aca ata gct gag gat gta tca gga atg cca gct ctg tgc tct cca att	1362		
Thr Ile Ala Glu Asp Val Ser Gly Met Pro Ala Leu Cys Ser Pro Ile			
410	415	420	
tcc cag gga ggg ggt ggt ttt gac tat cga cta gcc atg gca att cca	1410		
Ser Gln Gly Gly Gly Gly Phe Asp Tyr Arg Leu Ala Met Ala Ile Pro			
425	430	435	440
gat aag tgg att cag cta ctt aaa gag ttt aaa gat gaa gac tgg aac	1458		
Asp Lys Trp Ile Gln Leu Leu Lys Glu Phe Lys Asp Glu Asp Trp Asn			
445	450	455	
atg ggc gat ata gla tac acg ctc aca aac agg cgc tac ctt gaa aag	1506		
Met Gly Asp Ile Val Tyr Thr Leu Thr Asn Arg Arg Tyr Leu Glu Lys			
460	465	470	
tgc att gct tat gca gag agc cat gat cag gca ttg gtt ggg gat aag	1554		
Cys Ile Ala Tyr Ala Glu Ser His Asp Gln Ala Leu Val Gly Asp Lys			
475	480	485	
tcg ctg gca ttt tgg ttg atg gat gcc gaa atg tat aca aac atg agt	1602		
Ser Leu Ala Phe Trp Leu Met Asp Ala Glu Met Tyr Thr Asn Met Ser			
490	495	500	
gtc ctg act cct ttt act cca gtt att gat cgt gga ata cag ctt cat	1650		
Val Leu Thr Pro Phe Thr Pro Val Ile Asp Arg Gly Ile Gln Leu His			

505	510	515	520	
aaa atg att cga ctc att acg cat ggg ctt ggt gga gaa ggc tat ctc	1698			
Lys Met Ile Arg Leu Ile Thr His Gly Leu Gly Gly Glu Gly Tyr Leu				
525	530	535		
aat ttc atg ggt aat gaa ttt ggg cat cct gaa tgg tta gac ttc cca	1746			
Asn Phe Met Gly Asn Glu Phe Gly His Pro Glu Trp Leu Asp Phe Pro				
540	545	550		
aga aaa gga aat aat gag agt tac cat tat gcc agg cgg cag ttt cat	1794			
Arg Lys Gly Asn Asn Glu Ser Tyr His Tyr Ala Arg Arg Gln Phe His				
555	560	565		
tta act gac gac gac ctt ctt cgc tac aag ttc cta aat aat ttt gac	1842			
Leu Thr Asp Asp Asp Leu Leu Arg Tyr Lys Phe Leu Asn Asn Phe Asp				
570	575	580		
agg gat atg aat aga tlg gaa gaa aga tat ggt tgg ctt gca gct cca	1890			
Arg Asp Met Asn Arg Leu Glu Glu Arg Tyr Gly Trp Leu Ala Ala Pro				
585	590	595	600	
cag gcc tac gtg agt gaa aaa cat gaa ggc aat aag atc att gct ttt	1938			
Gln Ala Tyr Val Ser Glu Lys His Glu Gly Asn Lys Ile Ile Ala Phe				
605	610	615		
gaa aga gca ggt ctt ctt ttc att ttc aac ttc cat cca agc aag agc	1986			
Glu Arg Ala Gly Leu Leu Phe Ile Phe Asn Phe His Pro Ser Lys Ser				
620	625	630		
tac act gac tac cga gtt gga aca gca tlg cca ggg aaa ttc aaa att	2034			
Tyr Thr Asp Tyr Arg Val Gly Thr Ala Leu Pro Gly Lys Phe Lys Ile				
635	640	645		
gtg cta gal tca gat gca gcg gaa tat gga ggg cat cag aga ctg gac	2082			

Val Leu Asp Ser Asp Ala Ala Glu Tyr Gly Gly His Gln Arg Leu Asp
 650 655 660
 cac agc act gac ttt ttt tct gag gct ttt gaa cat aat ggg cgt ccc 2130
 His Ser Thr Asp Phe Phe Ser Glu Ala Phe Glu His Asn Gly Arg Pro
 665 670 675 680
 tat tct ctt ttg gtg tac att cca agc aga gtg gcc ctc atc ctt cag 2178
 Tyr Ser Leu Leu Val Tyr Ile Pro Ser Arg Val Ala Leu Ile Leu Gln
 685 690 695
 aat gtg gat ctg ccg aat tgaagaggcc tgatttcagc tccaccagat 2226
 Asn Val Asp Leu Pro Asn
 700
 gcagatttgt gttttgtttt ctgtttatca ctgtcacaca gcttataaca tgtatgcttt 2286
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 aatacagcaa acttttattt aagtagatag gagaatatgt ttaaaatatt aggaatccta 2406
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 gaattataac caaggtaata taaaagccat tacgtatgaa ctcatccgtg tctcatittg 2766
 tgttttattt tglgactct tgtccactaa gtaacttgtt aaatgccagt atctcagict 2826
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 aaaaagcttt tgt 2899

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<211> 702

<212> PRT

<213> Homo sapiens

<400> 106

Met Ala Ala Pro Met Thr Pro Ala Ala Arg Pro Glu Asp Tyr Glu Ala

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Ala Leu Asn Ala Ala Leu Ala Asp Val Pro Glu Leu Ala Arg Leu Leu

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Glu Ile Asp Pro Tyr Leu Lys Pro Tyr Ala Val Asp Phe Gln Arg Arg

35 40 45

Tyr Lys Gln Phe Ser Gln Ile Leu Lys Asn Ile Gly Glu Asn Glu Gly

50 55 60

Gly Ile Asp Lys Phe Ser Arg Gly Tyr Glu Ser Phe Gly Val His Arg

65 70 75 80

Cys Ala Asp Gly Gly Leu Tyr Ser Lys Glu Trp Ala Pro Gly Ala Glu

85 90 95

Gly Val Phe Leu Thr Gly Asp Phe Asn Gly Trp Asn Pro Phe Ser Tyr

100 105 110

Pro Tyr Lys Lys Leu Asp Tyr Gly Lys Trp Glu Leu Tyr Ile Pro Pro

115 120 125

Lys Gln Asn Lys Ser Val Leu Val Pro His Gly Ser Lys Leu Lys Val

130 135 140

Val Ile Thr Ser Lys Ser Gly Glu Ile Leu Tyr Arg Ile Ser Pro Trp

145 150 155 160

Ala Lys Tyr Val Val Arg Glu Gly Asp Asn Val Asn Tyr Asp Trp Ile

165 170 175

His Trp Asp Pro Glu His Ser Tyr Glu Phe Lys His Ser Arg Pro Lys

180 185 190

Lys Pro Arg Ser Leu Arg Ile Tyr Glu Ser His Val Gly Ile Ser Ser

195	200	205	
His Glu Gly Lys Val Ala Ser Tyr Lys His Phe Thr Cys Asn Val Leu			
210	215	220	
Pro Arg Ile Lys Gly Leu Gly Tyr Asn Cys Ile Gln Leu Met Ala Ile			
225	230	235	240
Met Glu His Ala Tyr Tyr Ala Ser Phe Gly Tyr Gln Ile Thr Ser Phe			
245	250	255	
Phe Ala Ala Ser Ser Arg Tyr Gly Thr Pro Glu Glu Leu Gln Glu Leu			
260	265	270	
Val Asp Thr Ala His Ser Met Gly Ile Ile Val Leu Leu Asp Val Val			
275	280	285	
His Ser His Ala Ser Lys Asn Ser Ala Asp Gly Leu Asn Met Phe Asp			
290	295	300	
Gly Thr Asp Ser Cys Tyr Phe His Ser Gly Pro Arg Gly Thr His Asp			
305	310	315	320
Leu Trp Asp Ser Arg Leu Phe Ala Tyr Ser Ser Trp Glu Val Leu Arg			
325	330	335	
Phe Leu Leu Ser Asn Ile Arg Trp Trp Leu Glu Glu Tyr Arg Phe Asp			
340	345	350	
Gly Phe Arg Phe Asp Gly Val Thr Ser Met Leu Tyr His His His Gly			
355	360	365	
Val Gly Gln Gly Phe Ser Gly Asp Tyr Ser Glu Tyr Phe Gly Leu Gln			
370	375	380	
Val Asp Glu Asp Ala Leu Thr Tyr Leu Met Leu Ala Asn His Leu Val			
385	390	395	400
His Thr Leu Cys Pro Asp Ser Ile Thr Ile Ala Glu Asp Val Ser Gly			

WO 01/25427

405 410 415
 Met Pro Ala Leu Cys Ser Pro Ile Ser Gln Gly Gly Gly Gly Phe Asp
 420 425 430
 Tyr Arg Leu Ala Met Ala Ile Pro Asp Lys Trp Ile Gln Leu Leu Lys
 435 440 445
 Glu Phe Lys Asp Glu Asp Trp Asn Met Gly Asp Ile Val Tyr Thr Leu
 450 455 460
 Thr Asn Arg Arg Tyr Leu Glu Lys Cys Ile Ala Tyr Ala Glu Ser His
 465 470 475 480
 Asp Gln Ala Leu Val Gly Asp Lys Ser Leu Ala Phe Trp Leu Met Asp
 485 490 495
 Ala Glu Met Tyr Thr Asn Met Ser Val Leu Thr Pro Phe Thr Pro Val
 500 505 510
 Ile Asp Arg Gly Ile Gln Leu His Lys Met Ile Arg Leu Ile Thr His
 515 520 525
 Gly Leu Gly Gly Glu Gly Tyr Leu Asn Phe Met Gly Asn Glu Phe Gly
 530 535 540
 His Pro Glu Trp Leu Asp Phe Pro Arg Lys Gly Asn Asn Glu Ser Tyr
 545 550 555 560
 His Tyr Ala Arg Arg Gln Phe His Leu Thr Asp Asp Asp Leu Leu Arg
 565 570 575
 Tyr Lys Phe Leu Asn Asn Phe Asp Arg Asp Met Asn Arg Leu Glu Glu
 580 585 590
 Arg Tyr Gly Trp Leu Ala Ala Pro Gln Ala Tyr Val Ser Glu Lys His
 595 600 605
 Glu Gly Asn Lys Ile Ile Ala Phe Glu Arg Ala Gly Leu Leu Phe Ile
 610 615 620

Phe Asn Phe His Pro Ser Lys Ser Tyr Thr Asp Tyr Arg Val Gly Thr
 625 630 635 640
 Ala Leu Pro Gly Lys Phe Lys Ile Val Leu Asp Ser Asp Ala Ala Glu
 645 650 655
 Tyr Gly Gly His Gln Arg Leu Asp His Ser Thr Asp Phe Phe Ser Glu
 660 665 670
 Ala Phe Glu His Asn Gly Arg Pro Tyr Ser Leu Leu Val Tyr Ile Pro
 675 680 685
 Ser Arg Val Ala Leu Ile Leu Gln Asn Val Asp Leu Pro Asn
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<210> 107

<211> 790

<212> DNA

<213> Homo sapiens

<220>

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<222> (78).. (626)

<400> 107

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 Met Thr Thr Ala Ser Thr Ser Gln Val Arg Gln
 1 5 10
 aac tac cac cag gac tca gag gcc gcc atc aac cgc cag atc aac ctg 158
 Asn Tyr His Gln Asp Ser Glu Ala Ala Ile Asn Arg Gln Ile Asn Leu
 15 20 25
 gag ctc tac gcc tcc tac gti tac ctg tcc atg tct tac tac ttt gac 206

Glu Leu Tyr Ala Ser Tyr Val Tyr Leu Ser Met Ser Tyr Tyr Phe Asp
 30 35 40
 cgc gat gat gtg gct ttg aag aac ttt gcc aaa tac ttt ctt cac caa 254
 Arg Asp Asp Val Ala Leu Lys Asn Phe Ala Lys Tyr Phe Leu His Gln
 45 50 55
 tct cat gag gag agg gaa cat gct gag aaa ctg atg aag ctg cag aac 302
 Ser His Glu Glu Arg Glu His Ala Glu Lys Leu Met Lys Leu Gln Asn
 60 65 70 75
 caa cga ggt ggc cga atc ttc ctt cag gat atc aag aaa cca gac tgt 350
 Gln Arg Gly Gly Arg Ile Phe Leu Gln Asp Ile Lys Lys Pro Asp Cys
 80 85 90
 gat gac tgg gag agc ggg ctg aat gca atg gag tgt gca tta cat ttg 398
 Asp Asp Trp Glu Ser Gly Leu Asn Ala Met Glu Cys Ala Leu His Leu
 95 100 105
 gaa aaa aat gtg aat cag tca cta ctg gaa ctg cac aaa ctg gcc act 446
 Glu Lys Asn Val Asn Gln Ser Leu Leu Glu Leu His Lys Leu Ala Thr
 110 115 120
 gac aaa aat gac ccc cat ttg tgt gac ttc att gag aca cat tac ctg 494
 Asp Lys Asn Asp Pro His Leu Cys Asp Phe Ile Glu Thr His Tyr Leu
 125 130 135
 aat gag cag gtg aaa gcc atc aaa gaa ttg ggt gac cac gtg acc aac 542
 Asn Glu Gln Val Lys Ala Ile Lys Glu Leu Gly Asp His Val Thr Asn
 140 145 150 155
 ttg cgc aag atg gga gcg ccc gaa tct ggc ttg gcg gaa tat ctc ttt 590
 Leu Arg Lys Met Gly Ala Pro Glu Ser Gly Leu Ala Glu Tyr Leu Phe
 160 165 170

gac aag cac acc cag gga gac agt gat aat gaa agc taagccctcgg 636

Asp Lys His Thr Leu Gly Asp Ser Asp Asn Glu Ser

175

180

gctaatttcc ccatagccgi ggggtgactt ccciggtcac caaggcagtg catgcatggt 696

ggggtttcct ttaccttttc tataagtgtg accaaaacat ccacttaagt tctttgattt 756

gtaccattcc ttcaaataaa gaaatttggg accc 790

<210> 108

<211> 183

<212> PRT

<213> Homo sapiens

<400> 108

Met Thr Thr Ala Ser Thr Ser Gln Val Arg Gln Asn Tyr His Gln Asp

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15

Ser Glu Ala Ala Ile Asn Arg Gln Ile Asn Leu Glu Leu Tyr Ala Ser

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25

30

Tyr Val Tyr Leu Ser Met Ser Tyr Tyr Phe Asp Arg Asp Asp Val Ala

35

40

45

Leu Lys Asn Phe Ala Lys Tyr Phe Leu His Gln Ser His Glu Glu Arg

50

55

60

Glu His Ala Glu Lys Leu Met Lys Leu Gln Asn Gln Arg Gly Gly Arg

65

70

75

80

Ile Phe Leu Gln Asp Ile Lys Lys Pro Asp Cys Asp Asp Trp Glu Ser

85

90

95

Gly Leu Asn Ala Met Glu Cys Ala Leu His Leu Glu Lys Asn Val Asn

100

105

110

Gln Ser Leu Leu Glu Leu His Lys Leu Ala Thr Asp Lys Asn Asp Pro

115 120 125
 His Leu Cys Asp Phe Ile Glu Thr His Tyr Leu Asn Glu Gln Val Lys
 130 135 140
 Ala Ile Lys Glu Leu Gly Asp His Val Thr Asn Leu Arg Lys Met Gly
 145 150 155 160
 Ala Pro Glu Ser Gly Leu Ala Glu Tyr Leu Phe Asp Lys His Thr Leu
 165 170 175
 Gly Asp Ser Asp Asn Glu Ser

180

<210> 109

<211> 3460

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (256).. (1857)

<400> 109

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 gggctgggct gtgcgccigc gcagtgtggg tcgctccga ttcctgccc cggccggccc 180
 cgcctcggct ccgcaccctc gcccgcctc cagccgccgc tctgccccgc agcagccagc 240
 cccgtgtccg gcagt atg ttc agc tgg gtc agc aag gat gcc cgc cgc aag 291

Met Phe Ser Trp Val Ser Lys Asp Ala Arg Arg Lys

1

5

10

aag gag ccg gag ctc ttc cag acg gtg gcc gag ggg ctg cgg cag ctg 339
 Lys Glu Pro Glu Leu Phe Gln Thr Val Ala Glu Gly Leu Arg Gln Leu

15	20	25	
tac gcg cag aag ctg cta ccc ctg gag gag cac tac cgc ttc cac gag	387		
Tyr Ala Gln Lys Leu Leu Pro Leu Glu Glu His Tyr Arg Phe His Glu			
30	35	40	
ttc cac tcg ccc gcr ctg gag gac gct gac ttc gac aac aag cct atg	435		
Phe His Ser Pro Xaa Leu Glu Asp Ala Asp Phe Asp Asn Lys Pro Met			
45	50	55	60
gtg ctc ctc gtg rgg cag tac agc acg ggc aag acc acc ttc atc cga	483		
Val Leu Leu Val Xaa Gln Tyr Ser Thr Gly Lys Thr Thr Phe Ile Arg			
65	70	75	
cac ctg atc gag cag gac ttc ccg ggg atg cgc atc ggg ccc gag ccc	531		
His Leu Ile Glu Gln Asp Phe Pro Gly Met Arg Ile Gly Pro Glu Pro			
80	85	90	
acc acc gac tcc ttc atc gcc gtc atg cac ggc ccc act gag ggc glg	579		
Thr Thr Asp Ser Phe Ile Ala Val Met His Gly Pro Thr Glu Gly Val			
95	100	105	
gtg ccg ggc aac gcg ctc gtg glg gac ccg cgg cgc ccc ttc cgc aag	627		
Val Pro Gly Asn Ala Leu Val Val Asp Pro Arg Arg Pro Phe Arg Lys			
110	115	120	
ctc aac gcg ttt ggc aac gct ttc ctc aac agg ttc atg tgt gcc cag	675		
Leu Asn Ala Phe Gly Asn Ala Phe Leu Asn Arg Phe Met Cys Ala Gln			
125	130	135	140
ctg ccc aac ccc gtc ctg gac agc atc agc atc atc gac acc ccc ggg	723		
Leu Pro Asn Pro Val Leu Asp Ser Ile Ser Ile Ile Asp Thr Pro Gly			
145	150	155	
atc ctg tct gga gag aag cag cgg atc agc aga ggc tat gac ttt gca	771		
Ile Leu Ser Gly Glu Lys Gln Arg Ile Ser Arg Gly Tyr Asp Phe Ala			

160	165	170	
gcc gtc ctg gag tgg ttc gcg gag cgt gtg gac cgc atc atc ctg ctc	819		
Ala Val Leu Glu Trp Phe Ala Glu Arg Val Asp Arg Ile Ile Leu Leu			
175	180	185	
ttc gac gcc cac aag ctg gac atc tcc gat gag ttc tcg gaa gtg atc	867		
Phe Asp Ala His Lys Leu Asp Ile Ser Asp Glu Phe Ser Glu Val Ile			
190	195	200	
aag gct ctg aag aac cat gag gac aag atc cgc gtg gtg ctg aac aag	915		
Lys Ala Leu Lys Asn His Glu Asp Lys Ile Arg Val Val Leu Asn Lys			
205	210	215	220
gca gac cag atc gag acg cag cag ctg atg cgg gtg tac ggg gcc ctc	963		
Ala Asp Gln Ile Glu Thr Gln Gln Leu Met Arg Val Tyr Gly Ala Leu			
225	230	235	
atg tgg tcc ctg ggc aag atc atc aac acc ccc gag gtg gtc agg gtc	1011		
Met Trp Ser Leu Gly Lys Ile Ile Asn Thr Pro Glu Val Val Arg Val			
240	245	250	
tac atc ggc tcc ttc tgg tcc cac ccg ctc ctc atc ccc gac aac cgc	1059		
Tyr Ile Gly Ser Phe Trp Ser His Pro Leu Leu Ile Pro Asp Asn Arg			
255	260	265	
aag ctc ttt gag gcc gag gag cag gac ctc ttc aag gac atc cag tca	1107		
Lys Leu Phe Glu Ala Glu Glu Gln Asp Leu Phe Lys Asp Ile Gln Ser			
270	275	280	
ctg ccc cga aac gcc gcc ctc agg aag ctc aat gac ctg atc aag cgg	1155		
Leu Pro Arg Asn Ala Ala Leu Arg Lys Leu Asn Asp Leu Ile Lys Arg			
285	290	295	300
gca cgg ctg gcc aag gtt cac gcc tac atc atc agc tcc ctc aag aaa	1203		

Ala Arg Leu Ala Lys Val His Ala Tyr Ile Ile Ser Ser Leu Lys Lys
305 310 315
gag atg ccc aat gtc ttt ggt aaa gag agc aaa aag aaa gag ctg gtg 1251
Glu Met Pro Asn Val Phe Gly Lys Glu Ser Lys Lys Lys Glu Leu Val
320 325 330
aac aac ctg gga gag atc tac cag aag att gag cgc gag cac cag atc 1299
Asn Asn Leu Gly Glu Ile Tyr Gln Lys Ile Glu Arg Glu His Gln Ile
335 340 345
tcc cct ggg gac ttc ccg agc ctc cgc aag atg cag gaa ctc ctg cag 1347
Ser Pro Gly Asp Phe Pro Ser Leu Arg Lys Met Gln Glu Leu Leu Gln
350 355 360
acc cag gac ttc agc aag ttc cag gcg ctg aag ccc aag ctg ctg gac 1395
Thr Gln Asp Phe Ser Lys Phe Gln Ala Leu Lys Pro Lys Leu Leu Asp
365 370 375 380
acg gtg gat gac atg ctg gcc aac gac atc gcg cgg ctg atg gtg atg 1443
Thr Val Asp Asp Met Leu Ala Asn Asp Ile Ala Arg Leu Met Val Met
385 390 395
gtg cgg cag gag gag tcc ctg atg cct tcc cag gtg gtc aag ggc ggc 1491
Val Arg Gln Glu Glu Ser Leu Met Pro Ser Gln Val Val Lys Gly Gly
400 405 410
gcc ttt gac ggc acc atg aac ggg ccg ttc ggg cac ggc tac ggc gag 1539
Ala Phe Asp Gly Thr Met Asn Gly Pro Phe Gly His Gly Tyr Gly Glu
415 420 425
ggg gcc ggc gag ggc atc cac gac gtg gag tgg gtg gtg ggc aag gac 1587
Gly Ala Gly Glu Gly Ile His Asp Val Glu Trp Val Val Gly Lys Asp
430 435 440
aag ccc acc tac gac gag atc ttc tac acg ctg tcc cct gtc aac ggc 1635

Lys Pro Thr Tyr Asp Glu Ile Phe Tyr Thr Leu Ser Pro Val Asn Gly
 445 450 455 460
 aag atc acg ggc gcc aac gcc aag aag gag atg gig aag tcc aag ctc 1683
 Lys Ile Thr Gly Ala Asn Ala Lys Lys Glu Met Val Lys Ser Lys Leu
 465 470 475
 ccc aac acc gtg cta ggg aag atc tgg aag ctg gcc gac gtg gac aag 1731
 Pro Asn Thr Val Leu Gly Lys Ile Trp Lys Leu Ala Asp Val Asp Lys
 480 485 490
 gac ggg ctg ctg gac gac gag gag ttc gcg ctg gcc aac cac ctc atc 1779
 Asp Gly Leu Leu Asp Asp Glu Glu Phe Ala Leu Ala Asn His Leu Ile
 495 500 505
 aag gtc aag ctg gag ggc cac gag ctg ccc gcc gac ctg ccc ccg cac 1827
 Lys Val Lys Leu Glu Gly His Glu Leu Pro Ala Asp Leu Pro Pro His
 510 515 520
 ctg gtg ccg ccc tcc aag cgc aga cat gag tgatggcgcc cggccccgca 1877
 Leu Val Pro Pro Ser Lys Arg Arg His Glu
 525 530
 cctgccattt gcacgcccgg ccgggaggca gagacggggg gaggggaagc ctcaccattt 1937
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<210> 110

<211> 534

<212> PRT

<213> Homo sapiens

<400> 110

Met Phe Ser Trp Val Ser Lys Asp Ala Arg Arg Lys Lys Glu Pro Glu

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10

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Leu Phe Gln Thr Val Ala Glu Gly Leu Arg Gln Leu Tyr Ala Gln Lys

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Leu	Leu	Pro	Leu
Glu	Glu	His	Tyr
Arg	Phe	His	Glu
Phe	His	Ser	Pro
	35	40	45
Xaa	Leu	Glu	Asp
Ala	Asp	Phe	Asp
Asn	Lys	Pro	Met
Val	Leu	Leu	Val
	50	55	60
Xaa	Gln	Tyr	Ser
Thr	Gly	Lys	Thr
Thr	Phe	Ile	Arg
His	Leu	Ile	Glu
	65	70	75
Gln	Asp	Phe	Pro
Gly	Met	Arg	Ile
Gly	Pro	Glu	Pro
Thr	Thr	Asp	Ser
	85	90	95
Phe	Ile	Ala	Val
Met	His	Gly	Pro
Thr	Glu	Gly	Val
Val	Pro	Gly	Asn
	100	105	110
Ala	Leu	Val	Val
Asp	Pro	Arg	Arg
Pro	Phe	Arg	Lys
Leu	Asn	Ala	Phe
	115	120	125
Gly	Asn	Ala	Phe
Leu	Asn	Arg	Phe
Met	Cys	Ala	Gln
Leu	Pro	Asn	Pro
	130	135	140
Val	Leu	Asp	Ser
Ile	Ser	Ile	Ile
Asp	Thr	Pro	Gly
Ile	Leu	Ser	Gly
	145	150	155
Glu	Lys	Gln	Arg
Ile	Ser	Arg	Gly
Tyr	Asp	Phe	Ala
Ala	Val	Leu	Glu
	165	170	175
Trp	Phe	Ala	Glu
Arg	Val	Asp	Arg
Ile	Ile	Leu	Leu
Phe	Asp	Ala	His
	180	185	190
Lys	Leu	Asp	Ile
Ser	Asp	Glu	Phe
Ser	Glu	Val	Ile
Lys	Ala	Leu	Lys
	195	200	205
Asn	His	Glu	Asp
Lys	Ile	Arg	Val
Val	Leu	Asn	Lys
Ala	Asp	Gln	Ile
	210	215	220
Glu	Thr	Gln	Gln
Leu	Met	Arg	Val
Tyr	Gly	Ala	Leu
Met	Trp	Ser	Leu
	225	230	235
			240

Gly Lys Ile Ile Asn Thr Pro Glu Val Val Arg Val Tyr Ile Gly Ser
245 250 255

Phe Trp Ser His Pro Leu Leu Ile Pro Asp Asn Arg Lys Leu Phe Glu
260 265 270

Ala Glu Glu Gln Asp Leu Phe Lys Asp Ile Gln Ser Leu Pro Arg Asn
275 280 285

Ala Ala Leu Arg Lys Leu Asn Asp Leu Ile Lys Arg Ala Arg Leu Ala
290 295 300

Lys Val His Ala Tyr Ile Ile Ser Ser Leu Lys Lys Glu Met Pro Asn
305 310 315 320

Val Phe Gly Lys Glu Ser Lys Lys Lys Glu Leu Val Asn Asn Leu Gly
325 330 335

Glu Ile Tyr Gln Lys Ile Glu Arg Glu His Gln Ile Ser Pro Gly Asp
340 345 350

Phe Pro Ser Leu Arg Lys Met Gln Glu Leu Leu Gln Thr Gln Asp Phe
355 360 365

Ser Lys Phe Gln Ala Leu Lys Pro Lys Leu Leu Asp Thr Val Asp Asp
370 375 380

Met Leu Ala Asn Asp Ile Ala Arg Leu Met Val Met Val Arg Gln Glu
385 390 395 400

Glu Ser Leu Met Pro Ser Gln Val Val Lys Gly Gly Ala Phe Asp Gly
405 410 415

Thr Met Asn Gly Pro Phe Gly His Gly Tyr Gly Glu Gly Ala Gly Glu
420 425 430

Gly Ile His Asp Val Glu Trp Val Val Gly Lys Asp Lys Pro Thr Tyr
435 440 445

Asp Glu Ile Phe Tyr Thr Leu Ser Pro Val Asn Gly Lys Ile Thr Gly

450

455

460

Ala Asn Ala Lys Lys Glu Met Val Lys Ser Lys Leu Pro Asn Thr Val

465

470

475

480

Leu Gly Lys Ile Trp Lys Leu Ala Asp Val Asp Lys Asp Gly Leu Leu

485

490

495

Asp Asp Glu Glu Phe Ala Leu Ala Asn His Leu Ile Lys Val Lys Leu

500

505

510

Glu Gly His Glu Leu Pro Ala Asp Leu Pro Pro His Leu Val Pro Pro

515

520

525

Ser Lys Arg Arg His Glu

530

<210> 111

<211> 1622

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (89).. (724)

<400> 111

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gtgtgattaa cctccatttc agctaatac atg gga gag att aaa gtc tct cct 112

Met Gly Glu Ile Lys Val Ser Pro

1

5

gat tat aac tgg ttt aga ggt aca gtt ccc ctt aaa aag att att gtg 160

Asp Tyr Asn Trp Phe Arg Gly Thr Val Pro Leu Lys Lys Ile Ile Val

10	15	20	
gat gat gat gac agt aag ata tgg tgc ctc tat gac gcg ggc ccc cga			208
Asp Asp Asp Asp Ser Lys Ile Trp Ser Leu Tyr Asp Ala Gly Pro Arg			
25	30	35	40
agt atc agg tgt cct ctc ata ttc ctg ccc cct gtc agt gga act gca			256
Ser Ile Arg Cys Pro Leu Ile Phe Leu Pro Pro Val Ser Gly Thr Ala			
45	50	55	
gat gtc ttt ttc cgg cag att ttg gct ctg act gga tgg ggt tac cgg			304
Asp Val Phe Phe Arg Gln Ile Leu Ala Leu Thr Gly Trp Gly Tyr Arg			
60	65	70	
gtt atc gct ttg cag tat cca gtt tat tgg gac cat ctc gag ttc tgt			352
Val Ile Ala Leu Gln Tyr Pro Val Tyr Trp Asp His Leu Glu Phe Cys			
75	80	85	
gat gga ttc aga aaa ctt tta gac cat tta caa ttg gat aaa gtt cat			400
Asp Gly Phe Arg Lys Leu Leu Asp His Leu Gln Leu Asp Lys Val His			
90	95	100	
ctt ttt ggc gct tct ttg gga ggc ttt ttg gcc cag aaa ttt gct gaa			448
Leu Phe Gly Ala Ser Leu Gly Gly Phe Leu Ala Gln Lys Phe Ala Glu			
105	110	115	120
tac act cac aaa tct cct aga gtc cat tcc cta atc ctc tgc aat tcc			496
Tyr Thr His Lys Ser Pro Arg Val His Ser Leu Ile Leu Cys Asn Ser			
125	130	135	
ttc agt gac acc tct atc ttc aac caa act tgg act gca aac agc ttt			544
Phe Ser Asp Thr Ser Ile Phe Asn Gln Thr Trp Thr Ala Asn Ser Phe			
140	145	150	
tgg ctg atg cct gca ttt atg ctc aaa aaa ata gtt ctt gga aat ttt			592
Trp Leu Met Pro Ala Phe Met Leu Lys Lys Ile Val Leu Gly Asn Phe			

155	160	165	
tca tct ggc ccg gtg gac cct atg atg gct gat gcc att gat ttc atg	640		
Ser Ser Gly Pro Val Asp Pro Met Met Ala Asp Ala Ile Asp Phe Met			
170	175	180	
gta gac agg cta gaa agt ttg ggt cag agt gaa ctg gct tca aga ctt	688		
Val Asp Arg Leu Glu Ser Leu Gly Gln Ser Glu Leu Ala Ser Arg Leu			
185	190	195	200
acc ttg aaa ttg tca aaa ttc tta tgt gga acc tca taaaattcgg	734		
Thr Leu Lys Leu Ser Lys Phe Leu Cys Gly Thr Ser			
205	210		
ggacatacct gtaactattta tggatgtgtt tgatcagagt gcgcatttcaa ctgaagctaa	794		
agaagaaaatg tacaagctgt atccctaattg ccccgaagag gctcatctga aaacaggagg	854		
caatttccca taccigtgca gaagtgcaga ggtaactctt tatgtacaga tacatttgtc	914		
kgcaattccw kggrggaccm aatacgcggc ctttgaccca tcaatggtea glgcccagga	974		
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<210> 112

WO 01/25427

<211> 212

<212> PRT

<213> Homo sapiens

<400> 112

Met Gly Glu Ile Lys Val Ser Pro Asp Tyr Asn Trp Phe Arg Gly Thr
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 Val Pro Leu Lys Lys Ile Ile Val Asp Asp Asp Asp Ser Lys Ile Trp
 20 25 30
 Ser Leu Tyr Asp Ala Gly Pro Arg Ser Ile Arg Cys Pro Leu Ile Phe
 35 40 45
 Leu Pro Pro Val Ser Gly Thr Ala Asp Val Phe Phe Arg Gln Ile Leu
 50 55 60
 Ala Leu Thr Gly Trp Gly Tyr Arg Val Ile Ala Leu Gln Tyr Pro Val
 65 70 75 80
 Tyr Trp Asp His Leu Glu Phe Cys Asp Gly Phe Arg Lys Leu Leu Asp
 85 90 95
 His Leu Gln Leu Asp Lys Val His Leu Phe Gly Ala Ser Leu Gly Gly
 100 105 110
 Phe Leu Ala Gln Lys Phe Ala Glu Tyr Thr His Lys Ser Pro Arg Val
 115 120 125
 His Ser Leu Ile Leu Cys Asn Ser Phe Ser Asp Thr Ser Ile Phe Asn
 130 135 140
 Gln Thr Trp Thr Ala Asn Ser Phe Trp Leu Met Pro Ala Phe Met Leu
 145 150 155 160
 Lys Lys Ile Val Leu Gly Asn Phe Ser Ser Gly Pro Val Asp Pro Met
 165 170 175

WO 01/25427

Met Ala Asp Ala Ile Asp Phe Met Val Asp Arg Leu Glu Ser Leu Gly

180

185

190

Gln Ser Glu Leu Ala Ser Arg Leu Thr Leu Lys Leu Ser Lys Phe Leu

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200

205

Cys Gly Thr Ser

210

<210> 113

<211> 2391

<212> DNA

<213> Homo sapiens

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<221> CDS

<222> (1).. (360)

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<221> unsure

<222> (49)

<223> g or t

<220>

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<222> (51)

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WO 01/25427

<221> unsure

<222> (55)

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<222> (1459)

<223> g or t

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<221> unsure

<222> (1705)

<223> g or t

<400> 113

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Asp Pro Phe His Ala Val Val Tyr Ile Val Phe Met Leu Gly Ser Cys

1

5

10

15

kcw tty kkc tcc aaa acg tgg att gag gtc tca ggt tcc tct scc aaa 96

Xaa Xaa Xaa Ser Lys Thr Trp Ile Glu Val Ser Gly Ser Ser Xaa Lys

20

25

30

gat gyt kca aag cag ctg aag gag cag cag atg gtg atg aga ggc cac 144

Asp Xaa Xaa Lys Gln Leu Lys Glu Gln Gln Met Val Met Arg Gly His

35

40

45

cga gag acc tcc atg gtc cat gaa ctc aac cgg tac atc ccc aca gcc 192

Arg Glu Thr Ser Met Val His Glu Leu Asn Arg Tyr Ile Pro Thr Ala

50

55

60

gcg gcc ttt ggt ggg ctg tgc atc ggg gcc ctc tcg gtc ctg gct gac 240

Ala Ala Phe Gly Gly Leu Cys Ile Gly Ala Leu Ser Val Leu Ala Asp
65 70 75 80
ttc cta ggc gcc att ggg tct gga acc ggg atc ctg ctc gca gtc aca 288
Phe Leu Gly Ala Ile Gly Ser Gly Thr Gly Ile Leu Leu Ala Val Thr
85 90 95
atc atc tac cag tac ttt gag atc ttc gtt aag gag yaa agc gag gtt 336
Ile Ile Tyr Gln Tyr Phe Glu Ile Phe Val Lys Glu Xaa Ser Glu Val
100 105 110
ggc agc atg ggg gcc ctg ctc ttc tgagcccgct tcccgacag gttaggaag 390
Gly Ser Met Gly Ala Leu Leu Phe
115 120
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<210> 114

<211> 120

<212> PRT

<213> Homo sapiens

<220>

<221> unsure

<222> (17)

<223> unknown

<220>

<221> unsure

<222> (18)

<223> unknown

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<220>

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<222> (109)

<223> unknown

<400> 114

Asp Pro Phe His Ala Val Val Tyr Ile Val Phe Met Leu Gly Ser Cys

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Xaa Xaa Xaa Ser Lys Thr Trp Ile Glu Val Ser Gly Ser Ser Xaa Lys

20 25 30

Asp Xaa Xaa Lys Gln Leu Lys Glu Gln Gln Met Val Met Arg Gly His

35 40 45

Arg Glu Thr Ser Met Val His Glu Leu Asn Arg Tyr Ile Pro Thr Ala

50 55 60

Ala Ala Phe Gly Gly Leu Cys Ile Gly Ala Leu Ser Val Leu Ala Asp

65 70 75 80
 Phe Leu Gly Ala Ile Gly Ser Gly Thr Gly Ile Leu Leu Ala Val Thr
 85 90 95
 Ile Ile Tyr Gln Tyr Phe Glu Ile Phe Val Lys Glu Xaa Ser Glu Val
 100 105 110
 Gly Ser Met Gly Ala Leu Leu Phe
 115 120

<210> 115

<211> 599

<212> DNA

<213> Homo sapiens

<400> 115

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 gctgctgggt ccttgttagc acaggagact tgggctaagg gccctccca gggaaggac 360
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<210> 116

<211> 364

<212> DNA

<213> Homo sapiens

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<221> unsure

<222> (134)

<223> a, c, g or t

<220>

<221> unsure

<222> (135)

<223> a, c, g or t

<220>

<221> unsure

<222> (179)

<223> g or a

<400> 116

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cacagttcca ggannggta ggtagcagtg tgtgtgttat gtgccactga ccctgaaara 180

tgtgccatag cccaagccaa ttgaaatga tcagggggcc aggcatggtg gctcatgcct 240

glaatcccag cacttggga agctgaggtg ggaggattgc ttgaaaccag gagttcaaga 300

ccagcctgig caacatagca aaaccccatc tctacaaaga ttaaaaataa aaaattagct 360

gggc

364

<210> 117

<211> 852

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (26).. (217)

<220>

<221> unsure

<222> (37)

<223> a, c, g or t

<400> 117

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Met Asp Gly Xaa Val Thr Phe Leu Thr

1

5

agc tgg gct aac ctt tcc cga act tgt ttc ccg gag gca agg tgc tcg 100

Ser Trp Ala Asn Leu Ser Arg Thr Cys Phe Pro Glu Ala Arg Cys Ser

10

15

20

25

gtg acc cag cgc atc tta acc ttg ggt ctc cta ggc tcg agg cta ggg 148

Val Thr Gln Arg Ile Leu Thr Leu Gly Leu Leu Gly Ser Arg Leu Gly

30

35

40

cat tac gtt tcg tgg aac caa agc agc caa ttg cat agc aag tat ttt 196

His Tyr Val Ser Trp Asn Gln Ser Ser Gln Leu His Ser Lys Tyr Phe

45

50

55

cct gca ttc caa tta aat gct taagaaaaag cagcatccta taaaattgtg 247

Pro Ala Phe Gln Leu Asn Ala

60

atcataaaca tccatttccc tcagcttttg tgagtgcctt gacttacagc caacatcact 307
 gtttaactca gtcgttttaa aaacaaactt ttctggtagg tgataacaga gatttgctcc 367
 ctgagccatc agggctctgg gagctggaag tgaaagggtt attaacattc taccittatg 427
 cagctgttgg ctgaccagaa taaactccct gctgagtcca agctttgaat ggaatggatg 487
 caaatgatgt tgtttccatt agagcaggtg ctacacagcat tctgattggc ctgagcagac 547
 cgaggctatg gctgttggga caagcttagc atcctggaca tcttgtcaaa gaacctcact 607
 caccctctg gcctctacag cctcagagg agagaaaacc aattctccaa caaacaggtc 667
 tctccaacat ggtgtgtctg gcaggcttag gtttagaaaa tctgactgt taaaggcgtt 727
 tgaatacatc acattcctat gcaaatgttt ttaatctcca gtttaatgta gtttattttt 787
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 gaagc 852

<210> 118

<211> 64

<212> PRT

<213> Homo sapiens

<220>

<221> unsure

<222> (4)

<223> unknown

<400> 118

Met Asp Gly Xaa Val Thr Phe Leu Thr Ser Trp Ala Asn Leu Ser Arg

1

5

10

15

Thr Cys Phe Pro Glu Ala Arg Cys Ser Val Thr Gln Arg Ile Leu Thr

20

25

30

Leu Gly Leu Leu Gly Ser Arg Leu Gly His Tyr Val Ser Trp Asn Gln

35

40

45

Ser Ser Gln Leu His Ser Lys Tyr Phe Pro Ala Phe Gln Leu Asn Ala

50

55

60

<210> 119

<211> 1156

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (524).. (1105)

<220>

<221> unsure

<222> (10)

<223> a or t

<400> 119

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 gctagagaca gggagagcag agtaaaaccc tcaggctgct gaaatttcta ggctgttagg 180
 aagcccctcg aattctgtga aaatgagggt ttcttaactc acactgagag cggaaagggg 240
 cagacccttt tcataactcc ctcaagtgig tgttaccttt cttaccagc atggttaagca 300
 acaggacata tcccagcctc ggacatgict gtagtatcca aggtacccaa agtcagacag 360
 agtaaaactca agcctggcac tggctttctg ccgcttcatg tgctttggaa aaagcaggag 420
 aagcaatagc agcaggagtc cccagcagct ggagccgcaa gaatgaactg caaagaggga 480
 actgacagca gctgcggctg cagggggcaa cgacgagaag aag atg ttg aag tgt 535

Met Leu Lys Cys

1

gtg gtg gtg ggg gac ggt gcc glg ggg aaa acc tgc ctg ctg atg agc 583
 Val Val Val Gly Asp Gly Ala Val Gly Lys Thr Cys Leu Leu Met Ser
 5 10 15 20
 tac gcc aac gac gcc ttc cca gag gaa tac gtg ccc act gtg ttt gac 631
 Tyr Ala Asn Asp Ala Phe Pro Glu Glu Tyr Val Pro Thr Val Phe Asp
 25 30 35
 cac tat gca gtt act gtg act gtg gga ggc aag caa cac ttg ctc gga 679
 His Tyr Ala Val Thr Val Thr Val Gly Gly Lys Gln His Leu Leu Gly
 40 45 50
 ctg tat gac acc gcg gga cag gag gac tac aac cag ctg agg cca ctc 727
 Leu Tyr Asp Thr Ala Gly Gln Glu Asp Tyr Asn Gln Leu Arg Pro Leu
 55 60 65
 tcc tac ccc aac acg gat gtg ttt ttg atc tgc ttc tct gtc gta aac 775
 Ser Tyr Pro Asn Thr Asp Val Phe Leu Ile Cys Phe Ser Val Val Asn
 70 75 80
 cct gcc tct tac cac aat gtc cag gag gaa tgg gtc ccc gag ctc aag 823
 Pro Ala Ser Tyr His Asn Val Gln Glu Glu Trp Val Pro Glu Leu Lys
 85 90 95 100
 gac tgc atg cct cac gtg cct tat gtc ctc ata ggg acc cag att gat 871
 Asp Cys Met Pro His Val Pro Tyr Val Leu Ile Gly Thr Gln Ile Asp
 105 110 115
 ctc cgt gat gac cca aaa acc ttg gcc cgt ttg ctg tat atg aaa gag 919
 Leu Arg Asp Asp Pro Lys Thr Leu Ala Arg Leu Leu Tyr Met Lys Glu
 120 125 130
 aaa cct ctc act tac gag cat ggt gtg aag ctc gca aaa gcg atc gga 967
 Lys Pro Leu Thr Tyr Glu His Gly Val Lys Leu Ala Lys Ala Ile Gly

135 140 145
 gca cag tgc tac ttg gaa tgt tca gct ctg act cag aaa ggt ctc aaa 1015
 Ala Gln Cys Tyr Leu Glu Cys Ser Ala Leu Thr Gln Lys Gly Leu Lys
 150 155 160
 gcg gtt ttt gat gaa gca atc ctc acc att ttc cac ccc aag aaa aag 1063
 Ala Val Phe Asp Glu Ala Ile Leu Thr Ile Phe His Pro Lys Lys Lys
 165 170 175 180
 aag aaa cgc tgt tct gag ggt cac agc tgc tgt tca att atc 1105
 Lys Lys Arg Cys Ser Glu Gly His Ser Cys Cys Ser Ile Ile
 185 190
 tgagggtgtc tgggacctgc ctccacccca tccagggatg agaatggcag c 1156

<210> 120

<211> 194

<212> PRT

<213> Homo sapiens

<400> 120

Met Leu Lys Cys Val Val Val Gly Asp Gly Ala Val Gly Lys Thr Cys
 1 5 10 15
 Leu Leu Met Ser Tyr Ala Asn Asp Ala Phe Pro Glu Glu Tyr Val Pro
 20 25 30
 Thr Val Phe Asp His Tyr Ala Val Thr Val Thr Val Gly Gly Lys Gln
 35 40 45
 His Leu Leu Gly Leu Tyr Asp Thr Ala Gly Gln Glu Asp Tyr Asn Gln
 50 55 60
 Leu Arg Pro Leu Ser Tyr Pro Asn Thr Asp Val Phe Leu Ile Cys Phe
 65 70 75 80

Ser Val Val Asn Pro Ala Ser Tyr His Asn Val Gln Glu Glu Trp Val
 85 90 95
 Pro Glu Leu Lys Asp Cys Met Pro His Val Pro Tyr Val Leu Ile Gly
 100 105 110
 Thr Gln Ile Asp Leu Arg Asp Asp Pro Lys Thr Leu Ala Arg Leu Leu
 115 120 125
 Tyr Met Lys Glu Lys Pro Leu Thr Tyr Glu His Gly Val Lys Leu Ala
 130 135 140
 Lys Ala Ile Gly Ala Gln Cys Tyr Leu Glu Cys Ser Ala Leu Thr Gln
 145 150 155 160
 Lys Gly Leu Lys Ala Val Phe Asp Glu Ala Ile Leu Thr Ile Phe His
 165 170 175
 Pro Lys Lys Lys Lys Lys Arg Cys Ser Glu Gly His Ser Cys Cys Ser
 180 185 190
 Ile Ile

<210> 121

<211> 1732

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (2).. (259)

<220>

<221> unsure

<222> (28)

<223> a, c, g or t

<220>

<221> unsure

<222> (388)

<223> g or a

<220>

<221> unsure

<222> (631)

<223> a or t

<220>

<221> unsure

<222> (637)

<223> g or a

<220>

<221> unsure

<222> (638)

<223> g or a

<220>

<221> unsure

<222> (639)

<223> g or a

<400> 121

g gac att gag tcc aag gag cag gtg cgn acc ctc acg ggc cac gtg ggc 49

Asp Ile Glu Ser Lys Glu Gln Val Xaa Thr Leu Thr Gly His Val Gly

1

5

10

15

acc gig tai gcc ctg gcg gtc atc tcg acg cca gac cag acc aaa gtc 97

Thr Val Tyr Ala Leu Ala Val Ile Ser Thr Pro Asp Gln Thr Lys Val

20 25 30
 ttc agt gca tcc tac gac cgg tcc ctc agg gtc tgg agt atg gac aac 145
 Phe Ser Ala Ser Tyr Asp Arg Ser Leu Arg Val Trp Ser Met Asp Asn
 35 40 45
 atg atc tgc acg cag acc ctg ctg cgt cac cag ggc agt gtc acc gcg 193
 Met Ile Cys Thr Gln Thr Leu Leu Arg His Gln Gly Ser Val Thr Ala
 50 55 60
 ctg gct gtg tcc cgg ggc cga ctc ttc tca ggg gct gtg gat agc act 241
 Leu Ala Val Ser Arg Gly Arg Leu Phe Ser Gly Ala Val Asp Ser Thr
 65 70 75 80
 gtg aag gtt tgg act tgc taacaggatc caggccaggc tgtggtttcc 289
 Val Lys Val Trp Thr Cys
 85
 cctgaaccag cccigggacct ttcigagcca ggcigggccac atggggtggt ctgggggttt 349
 ctgccigccc cgtgggcata ggtggacagg ctctggcarg cgggcagtgc cctccccgtc 409
 ccatgctcgg cgagcctccc tctactcggc actgtccttg ctgccagacc cctctciggg 469
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 gaggaaggac cgcaggcaga cagccctggc ctctaacagc tttgtccgg agctagactt 1669
 cgtgtccitt cagtiggtaa atggtttct atagaatcaa taatattct tcttttaa 1729
 ata 1732

<210> 122

<211> 86

<212> PRT

<213> Homo sapiens

<220>

<221> unsure

<222> (9)

<223> unknown

<400> 122

Asp Ile Glu Ser Lys Glu Gln Val Xaa Thr Leu Thr Gly His Val Gly

1 5 10 15

Thr Val Tyr Ala Leu Ala Val Ile Ser Thr Pro Asp Gln Thr Lys Val

20 25 30

Phe Ser Ala Ser Tyr Asp Arg Ser Leu Arg Val Trp Ser Met Asp Asn

35 40 45

Met Ile Cys Thr Gln Thr Leu Leu Arg His Gln Gly Ser Val Thr Ala

50

55

60

Leu Ala Val Ser Arg Gly Arg Leu Phe Ser Gly Ala Val Asp Ser Thr

65

70

75

80

Val Lys Val Trp Thr Cys

85

<210> 123

<211> 603

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (168).. (350)

<220>

<221> unsure

<222> (343)

<223> g or a

<220>

<221> unsure

<222> (422)

<223> t or c

<220>

<221> unsure

<222> (457)

<223> g or c

<400> 123

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 acagatgtga cccaggctta cttaaagagac aatccacag cctgggaac acactcttga 120
 gccaaacttg gtgaagaci aggtcttccc tggcaagttc cggaaga atg gac tta 176

Met Asp Leu

1

ctg act ttt atc aac tct tct cac tgc caa ggc caa cag cat ctg agg 224
 Leu Thr Phe Ile Asn Ser Ser His Cys Gln Gly Gln Gln His Leu Arg

5

10

15

tat agc ttt ttg gga gta cct gct ttc ttg cct cct gga gga tat ttt 272
 Tyr Ser Phe Leu Gly Val Pro Ala Phe Leu Pro Pro Gly Gly Tyr Phe

20

25

30

35

ctg tcc tgg ggc ttc atg gcc cct ctc ttc cct gtt aca cat tgc tgt 320
 Leu Ser Trp Gly Phe Met Ala Pro Leu Phe Pro Val Thr His Cys Cys

40

45

50

gct tca gag cct ttg cag ctg cra cct agt tgaatccaca taggsttcc 370
 Ala Ser Glu Pro Leu Gln Leu Xaa Pro Ser

55

60

tccacacggt gggaaggatc ttgctgcitt cactcacagg accaggaggat tyttcaatca 430
 ggaggtgggt ttttgttccc ttcaggscit tggcaacatc tagagacagt ttigtattgcc 490
 acgcctggag tgggaigtgt gtgctactgg catctagtgg ctgctaaaca tcciacactg 550
 cataggatag tccccactac cccagccaa gaattatctg actccagggg tca 603

<210> 124

<211> 61

<212> PRT

<213> Homo sapiens

<220>

<221> unsure

<222> (59)

<223> unknown

<400> 124

Met Asp Leu Leu Thr Phe Ile Asn Ser Ser His Cys Gln Gly Gln Gln

1 5 10 15

His Leu Arg Tyr Ser Phe Leu Gly Val Pro Ala Phe Leu Pro Pro Gly

20 25 30

Gly Tyr Phe Leu Ser Trp Gly Phe Met Ala Pro Leu Phe Pro Val Thr

35 40 45

His Cys Cys Ala Ser Glu Pro Leu Gln Leu Xaa Pro Ser

50 55 60

<210> 125

<211> 1289

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (775).. (1017)

<220>

<221> unsure

<222> (200)

<223> g or a

<400> 125

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ctttatagga aactattttt taaaaaaagc catttccac ccaaggacac agtggatgtg 120

ttttccctga ctccagcagg gcaaggaatg taaccgagag gttgtgtggg ctgggctctg 180
 gtgccctctt cccitggcccr gaacacctct cctcctgatt cccitggcac ctgtcttttc 240
 tgtctgttta cctgtctccc tgcctgcca tctgcatctt ttgcagccca ctctgacttc 300
 catctggggg ctgagaccac ccttgccctgc ccccttcttt ctgcctlaag aatgtccctt 360
 taggctgggc atggttgtca cgcctgtaac cccagcactt tgggaggcgg agacgggcag 420
 ataacctgag gtcaggattt cgagaccaac ctgacctaca tggagaaact ccgcctctag 480
 taaaaataca aaattagccg ggcatggltg tgcacgcctc taatcccagc tactcgggag 540
 gctgaggcag gagaatcact tgaacccggg aagtggaggt tgcagtgagc caagagtaca 600
 ccactgcact ccagcctggg caacagagcg agactccgc ttaaaaaaaaa aaaaaaaaaag 660
 aagcccttt tactgtctc atcatcccag tttagggcag tgcctggagt gggaaggccg 720
 tcttagacca tagaggttg aagacgtga gagatcatcc agcccagccc ctig atg 777

Met

1

tta cag agc aga aga cag atg ccc aaa cag gag aag gca ctt gcc cac 825
 Leu Gln Ser Arg Arg Gln Met Pro Lys Gln Glu Lys Ala Leu Ala His

5

10

15

ggt cat acg gca ggt tgc cac aaa acc aag atg gca gcc ctt cct cag 873
 Gly His Thr Ala Gly Cys His Lys Thr Lys Met Ala Ala Leu Pro Gln

20

25

30

cgt gcc tca ctg cca ctc cca gag cca ggg agc ccc ata aaa ccc aca 921
 Arg Ala Ser Leu Pro Leu Pro Glu Pro Gly Ser Pro Ile Lys Pro Thr

35

40

45

tca tgl ctt aag agt ata tct ggc tcc ttg acc agc aat cgg ccc tgg 969
 Ser Cys Leu Lys Ser Ile Ser Gly Ser Leu Thr Ser Asn Arg Pro Trp

50

55

60

65

gag cca cca ggt ggg aaa agc gcc tct gcc aga gtc cag gcc ttg gga 1017

Glu Pro Pro Gly Gly Lys Ser Ala Ser Ala Arg Val Gln Ala Leu Gly

70

75

80

tgacagacag ctgccccga cactcgggcc ccactcaagg atgtagggcc tttcttggcc 1077

cctgaccctt ccctgggcat tgggagcgtg gggacggggc tggccttggg aggagcggca 1137

ggggcattcac ctcccttctgc tgccttcccc tgcctcctacc ctcaagggcc tgggggctgc 1197

ccagctgcct ctatgccctt ctgggggtct cagccctactg ctgacacttc tgcaatccag 1257

agaaacacta aataaagcaa tacgtgtttg cc 1289

<210> 126

<211> 81

<212> PRT

<213> Homo sapiens

<400> 126

Met Leu Gln Ser Arg Arg Gln Met Pro Lys Gln Glu Lys Ala Leu Ala

1

5

10

15

His Gly His Thr Ala Gly Cys His Lys Thr Lys Met Ala Ala Leu Pro

20

25

30

Gln Arg Ala Ser Leu Pro Leu Pro Glu Pro Gly Ser Pro Ile Lys Pro

35

40

45

Thr Ser Cys Leu Lys Ser Ile Ser Gly Ser Leu Thr Ser Asn Arg Pro

50

55

60

Trp Glu Pro Pro Gly Gly Lys Ser Ala Ser Ala Arg Val Gln Ala Leu

65

70

75

80

Gly

<210> 127

<211> 1085

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (734).. (886)

<220>

<221> unsure

<222> (276)

<223> g or t

<400> 127

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ggaattacag gcacgcacca ccatgcciga ctaattttgt atttttagta gacatggggt 180
ttctccatgt tggctaggct gggtcacaac tcccacctic aggtgatccg cccacctcgg 240
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aagtigaagg caattcttca catgtaaaca gtgccagtgc acagaacctt tatatatatt 360
ttgaagccag tactgtgctc tgcatataac aaagctgctt caaggatgag acctttttct 420
aaaagcatgt aatgtgagaa gccggcctgc cttattttct ttttctttt ttaatgatta 480
aaaatagttt gtggcaaggc acgglggctc aggcctgtaa ttctagcact ttgggaggcc 540
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actgcatctc tacagagagt aaaaaaatt acccgagtgt ggtgatgtgc atctgtaac 660
tcagctactt gggaggctga ggtgagagga tcacttgagc ttgggtgagg tgaggctgca 720
gtgagtcctg atc atg ctg ctg cac tca atc ttg gac aac aga gca aga 769

```

Met Leu Leu His Ser Ile Leu Asp Asn Arg Ala Arg

1

5

10

```

ccc tgt ctc aaa aaa aaa aaa aat ata tat ata tat ata tat tat ttt 817

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Pro Cys Leu Lys Lys Lys Lys Asn Ile Tyr Ile Tyr Ile Tyr Tyr Phe
 15 20 25
 tat gag gtc aag tgc atc aaa ctt ggg aaa gat ttg agg agg ctg gga 865
 Tyr Glu Val Lys Cys Ile Lys Leu Gly Lys Asp Leu Arg Arg Leu Gly
 30 35 40
 acc tcc tgg aaa acc act cct tgaagaaaga tatgagagac atttagaagt 916
 Thr Ser Trp Lys Thr Thr Pro
 45 50
 gattccctgct ttcagaagga ggtggattca aatacatcaa aagtccttcc ctctgctaag 976
 tgtttatagt tcaatgaata atttcaatat ttgtatgigt tcttgctatt ttattttttt 1036
 ctgaaaaact tccaaaaatt tgaaaataaa attacagcct tttcttctt 1085

<210> 128

<211> 51

<212> PRT

<213> Homo sapiens

<400> 128

Met Leu Leu His Ser Ile Leu Asp Asn Arg Ala Arg Pro Cys Leu Lys
 1 5 10 15
 Lys Lys Lys Asn Ile Tyr Ile Tyr Ile Tyr Tyr Phe Tyr Glu Val Lys
 20 25 30
 Cys Ile Lys Leu Gly Lys Asp Leu Arg Arg Leu Gly Thr Ser Trp Lys
 35 40 45
 Thr Thr Pro
 50

<210> 129

<211> 1544

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> (1076)

<223> g or a

<400> 129

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acaaaaaccc aattttgttc atatigaagc atgaaataaa tgagagcaag glagggccaa 180

attaactctt gtggacagtc cctaaaagtc cagtcttaca ttgtgaaaa ttgtggtgcc 240

atgaattaag atggatgact ggaaaaaggt gtggagaaa gagttaaaga tgaggaagag 300

atatttttag tataatgaagt taaccaggga ctgataatc ataattcagt gctgtggaaa 360

tgaaaaaaat gatigaagag gtggaacgga aatgacctta gggggaaaaa aaaggaccaa 420

agaagctga ttaaaagtig aaatcagtat ttctgaattc aaattgcttg aatttccaaa 480

atagtcagta aaggatctaa tagaaccaga attatttggg tgaattctgc aggttttatg 540

ggcttgtcac aacgtgaagg gctggaatgt atattaccaa atgggaattt ccattgtagg 600

tttttgctag tcccaccccc attttagcct aatttggcct aaacgcagta tggggagaat 660

tgltcccat ccatgtgtc tgaattcagc tcatctccca gcatatagat atatcctcct 720

ttaactccga ccagaacct tcttctgtg gcactcccca ccatagacc ttcagaicat 780

ctcccacacc ctggatctca ctctcctctt agtaacagag acactcctga ggttggactt 840

ccctgctttt ctctacttcc aaatcacaat ttcttacaac caagctttgt gctcccagat 900

aagcagggat gtactagggg aatgtaaaac tgcaaaccta aaaacctgca tcttcttgaa 960

gcalcagttt tacttaccaa atggtttaga gtcataagat gacctatctt tatataaaag 1020

ttatattata gaataaaaig ttcatagca tagactgtta agataaaaaa ataggraatc 1080

tigcaaggta attcttattt gcaagtgggt tatgtgttca ctctcctcta cctttatggt 1140

attttgggtg tcacttacga agcatacaac tagaaccata tccaagcaga ctctgggttg 1200

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ttaggaccag ctgattgtta tgcctgcagg atggttttga aacagaaaca atacttgttt 1380

actgtaggaa tcctatitai attatititc agtcctgiga atgctgigaa aagattitatt 1440

ccittgaggc caggaagctc ccaggcatai atgcttctag gttaggattg tcctgactca 1500

ctaaagaigc caggatattg gggctgaggg gagtttgagg tggt 1544

<210> 130

<211> 508

<212> DNA

<213> Homo sapiens

<400> 130

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atgggaaaca ggttatcggg ggattcatga agtcagttag agtaattgct tcttttttgc 120

gggtgaactg aatgtatttc ttcaccaaatt cttagatgta acaattaaaa agaagaaatg 180

acatgcaagt aggtcttagc agaaaaatgc aggcctgggca tgagtcatgt tgttaccctc 240

ccacatgctc ctacaatcca cagagatgcc tgtctgcagg ttctigaagt tattgttagt 300

atttggtatc tcaaatitit cgtcactgtt cacatgccac ttctctctg cacagtggta 360

tcctcatttg ctttttaacc tacactgagg agtccttctc aggttgcact gattttccaa 420

ttctgcagta atgagtaagc tcacggcatg gggaagaaga cagtcagtcc aatgaagttc 480

tctaaattat tttaacattg cctttgaa

508

<210> 131

<211> 1204

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> (50)

<223> g or t

<220>

<221> unsure

<222> (54)

<223> g or c

<220>

<221> unsure

<222> (300)

<223> g or c

<220>

<221> unsure

<222> (407)

<223> g or a

<220>

<221> unsure

<222> (415)

<223> a, c, g or t

<220>

<221> unsure

<222> (417)

<223> g or c

<220>

<221> unsure

<222> (419)

<223> t or c

<220>

<221> unsure

<222> (430)

<223> a or t

<220>

<221> unsure

<222> (448)

<223> t or c

<220>

<221> unsure

<222> (449)

<223> g or t

<220>

<221> unsure

<222> (472)

<223> a, c, g or t

<400> 131

ggccccctggc aaattgccctc aagatggggg ttigaaaata actttaccik actsaaggag 60

tgctcggagc accicctagt ctaagictgc aagctccagt tcttgcctaa aaccaatgcc 120

gtggccacc cttgggtcag acagctctgg gccctttgac cacaagccag cccctcggcc 180

tctcctggc atagcttct ctgccccagg actgcagggc ggcttcctcc aaggcttcca 240

aggtcaaaa gaaatttggc tccatccaag aaggctccag ctccccctact ggccccctggs 300

ttcaggccca cacccttggg ccagggccag agagtgtgtc tcaggagaa tcaatgggct 360

ctagagagac acacagaaag ttggggcatt tgggaaattt tcaaggrtgt atgtntsgyt 420

cacgtatggw gcaggttgtc ctggctcykg ggtgcaggga agtgggctgc anggaagtgg 480

attggagggg agcttgagga atataaggag cgggggttga gactcaggct atggacaagg 540

acagcccaa ggttgggaag acctggcctt agtcgtctc agcctagggg cagggcagtg 600

aagaaagctc tccccgtcc tgcgtaatg acccagagta gcctccccag gccggcatct 660

tatgtgtgtc ttccaccatc ctcatggttg cacttttcta ggctgtctc ccagcattgt 720

gcaaggctcg gaagagaacc aggaagtga aactgggtga aaacagaaag ctcaatggat 780

gggctagggt cccagatca ttagggcaga gtttgacgt cctctggta ctggaatcca 840

cccagccac gaatcalctc cctctgaag gattttattt ctactgggt ttggaacaaa 900

ctcctgctga gacccacag ccagaaactg aaagcagcag ctcccaaag cctggaaaat 960

ccctaagaga aggcctgggg caggaagtgg agtgacaggg gacagglaga gagaaggggg 1020

cccaatggcc agggagtga ggaggtggcg ttgctgagag cagtctgcac atgcttctgt 1080

ctgagtcag gaaggtgttc cagggtcgaa attacacttc tcgtacctgg agacgctgtt 1140

tgtagggagca ctgggctcat gcciggcaca caataggct gcaataaacc atggttaaat 1200

cctg 1204

<210> 132

<211> 508

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> (223)

<223> a, c, g or t

<220>

<221> unsure

<222> (237)

<223> a, c, g or t

<220>

<221> unsure

<222> (380)

<223> a, c, g or t

<220>

<221> unsure

<222> (468)

<223> a, c, g or t

<400> 132

cccgggagaa tcacttcagc ctgggagatc aaggctgcag tgagctctga acgcaccact 60

acactccagc ctgggtgaca gactgagatc ctgtctcaaa aaaagagaaa gaaaaccttt 120

gagattcttc catTTTTaga gctgagagag cacttgtgaa acacacacac atgcacaaac 180

atataaacat gcatacaggc atgcacatgc acacacaaat acncatacac acacacnagc 240

acacacacac caccaccacc atcatcagag gaacttacag aaaaggggac atttatagat 300

tcctaggaat atgccaaagc ttttcaaagc ctctatggac agctcatlcc ttaacttttc 360

ctcttttaaaa tcttttttan cttctttattt gccccagcca ctatcactgc ctccaggcagc 420

tgcaacglla aacaattgcc actgattact ttcaacaaat aacctcanag aaaaggctgt 480

gtgtattgaa tgggtatcaa gtcacgic

508

<210> 133

<211> 484

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> (313)

<223> a, c, g or t

<220>

<221> unsure

<222> (336)

<223> g or c

<220>

<221> unsure

<222> (401)

<223> g or c

<400> 133

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tcttgagag ggatggagac tgaagagta gtttggtcct ccacttgatc caggttctta 120

ttttgtttt ctacttcaaa gcgagaactt ggtactgtga ctttgataag aattgacttc 180

aggcccagca agatccctca tgccigtat cccagcactt tggggggcca aggcaggagg 240

attgcgtgag cccaggagtt cgagaccac ctgggcaaca tagggaccit gtctctacaa 300
aaaataaaat tanciggggt tgaiggtgca catcastggt cctggctact cgggaggcca 360
aggtagggagg aatgcttgag gatcggaggt caaggctgca sigagccaat attgtgccac 420
tgcatccag cctgggcaac agagigagac actgtctta aaaaaaaaaa aaaaaacgt 480
ccgc 484

<210> 134

<211> 605

<212> DNA

<213> Homo sapiens

<400> 134

gctgcatgtc taaaattaca tggagttagt gctattctt ttcccccctt tgcagcaact 60
tacacagcat tttaacacc tttttttct agttttttg ttgggtttg ttcccatca 120
ggaatttgag ttctctctaa cccagcttac tggggacat agaaaaactc agtagaaata 180
ccttgggtga tcttggtgag ttaagtctg atcttgatc taaactcagt aagccactat 240
ctgcaatttt gtacattata tagtattttg aagataatga accttatgaa aaaaaaatag 300
caaattagtt ctttttccc cagaggggaa agtatgttc tgcaaatagt gigtgtctta 360

WO 01/25427

ttttactgtt gaacagcaat tgctatttat ttttttatlg cctagaactt caacatgttg 420
 tataggaatc ctgtagtgcc actagttaaa tgccgaattc tcatctggat gttaccaalca 480
 aacatcaglia cacttgteat ttcacatgig tttaatgiga cagtttttca gtacigtatg 540
 tgtaatttc tacttttttt aatatttaaa attgctttta aataaacata ttctcagttg 600
 atccc 605

<210> 135

<211> 1786

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (2).. (151)

<220>

<221> unsure

<222> (689)

<223> g or a

<400> 135

g gca cga ggg tcc tct gca tgg ggt cag gtg ctt ctg tgc ttg ctg tcc 49

Ala Arg Gly Ser Ser Ala Trp Gly Gln Val Leu Leu Cys Leu Leu Ser

1

5

10

15

tac ctc tct cca cag cag ggc tct caa aac cat ttt gat ccc cca ttg 97
 Tyr Leu Ser Pro Gln Gln Gly Ser Gln Asn His Phe Asp Pro Pro Leu
 20 25 30
 gca gag ggt tcc cct ctt tac aga gtt cag tca tta aaa gca tgg atc 145
 Ala Glu Gly Ser Pro Leu Tyr Arg Val Gln Ser Leu Lys Ala Trp Ile
 35 40 45
 agc tgt taatctcatt ggaggaggga actgtttcct gcattcattc atctgggaac 201
 Ser Cys
 50
 ctctcttgagt agccactgtc tgccagccac tgctctagag atgggaaaac agcacggaac 261
 aaaaccaagg tcctttctcc agcgaattta tatccttcag gaagctgggt cctgccacca 321
 acttagcagg caacagttct cctcccctag tgggcacagg gtaccagtgt ttaggaaaa 381
 gtggtccagc aaaggaagaa agcagaccaa ccagctgcc ttaccttatt ctggggccat 441
 tccccagcg atgagagctg cctctgtttc tactgccacc atctcttcig gctgcattc 501
 acctgctgct tgagcttcig accttccctc agttccacca aatgaggaca ggaatagca 561
 glcaagaccc ctgggccctg ctgagcgtga aacaggaagg caatgggatg agttgctggg 621
 acggaagaat gggcctgggg cagaacaaat agggagcatt tgaagcttc tggctgataa 681
 atctccargg tgcattccgg ttgccagcc tgcacctt aacctgctcc tggtaaatac 741
 tgatccagca gctgctccag gagaggccgt ctttttttc ccagccacgc tgtgtctttg 801
 catgagactc ctggggcctt gggcacagag agaaaagaat tgagactcag gaggtcaggt 861
 gggtagaaaa atgcaaagtg gcttcacaga cacagggtg tgggagcaga tcgacgggga 921
 acttgggaga tgaacttcag ggccttccga cgcttgtct caggaacatg ctttagaaaa 981
 aatggttagca tcctttccat aactcagttc ctcttcccta gtttccctga agtgtgacgt 1041
 tttagtatct ggagctcagt gatcccatg aatgagggat aaagtttcac tcttggtatt 1101
 ttctaactag tgctagggaa agtctgaga cagatcaca gccactgctt ggcatacagg 1161
 gcctccaccc aataagcaaa ctggagattc ctacgctct cgtggacacc cacatctcat 1221

tcttctcaca gcagagaagc tctcccttca gccctgagctg tcttcttctt gctgcagtg 1281
 agccctgctcc ctcttacctt ggccctcaagg aaggctggaa acatcttctg catttcaaag 1341
 tcttcacttt gacttatttg gccttcatct tggcatggaa ggtggcaggc agaattggaaa 1401
 tacciccccc caaacaaaac agatattctt gcgigtgtaa gggcagaagg gacaagctct 1461
 ctatcccatg agactagggg ccggagccca cctgcctttc cccacaactt ttcctgctca 1521
 aaccctctcc tcttgacaca ctggaatctg tattatata atttttaaga aaatacaatg 1581
 atgggtgtct ggttttgttg tttttacagg tglgttgtaa taaaaactgt aagaaaatta 1641
 agtatttaaa atgttccaat aaagtggggt ttttgttat tctaataat tattgtgtac 1701
 ctattgtaaa tatgaaacac tcttattttg caagctgagg acacaatttg tactgttgtt 1761
 atatataaat aaagtttact gaatt 1786

<210> 136

<211> 50

<212> PRT

<213> Homo sapiens

<400> 136

Ala Arg Gly Ser Ser Ala Trp Gly Gln Val Leu Leu Cys Leu Leu Ser

1 5 10 15

Tyr Leu Ser Pro Gln Gln Gly Ser Gln Asn His Phe Asp Pro Pro Leu

20 25 30

Ala Glu Gly Ser Pro Leu Tyr Arg Val Gln Ser Leu Lys Ala Trp Ile

35 40 45

Ser Cys

50

<210> 137

<211> 835

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (535).. (729)

<400> 137

gaaaaatcic attatttcaa aatgatagac atataccaaa aacaagtcta taatgtagt 60
 agtlactaaa attiacacat cttaaaagtg tgtaaatgct taaatttcag aattaccatc 120
 agaaccitcaa ttgacattcc tttgaatagg ctaataagtg acaataaga ttaataagat 180
 ttttcaaaat cgccaggact ggtgaatala aatgatgatt gaactggaat aatatigggg 240
 accaaatcaa atgaatgatt aaattatgaa gctcatatcc ttttgaaggt agttgcaaag 300
 agacatttca aaactgcctt aggccattgc agcatcctta gatgggacgc ataalcatta 360
 ccttaaagca tcaccactca tttigacatc atagatttta ttatgttagt ttaaaaggtc 420
 aatcagcctc atgactttat agttatgtct tgtattttaa aacatttttt atacatttgg 480
 ttaigttagt aaacaaaaaa catttgatta ataaaatata tatttgaata aatt atg 537

Met

1

agc tat cct ttc aaa cag cta ttg gca agt ttt aaa ccc aaa ata tat 585

Ser Tyr Pro Phe Lys Gln Leu Leu Ala Ser Phe Lys Pro Lys Ile Tyr

5

10

15

aca cat agt tct gta ata aaa ctg ttt gac ttc tca agt aac atg act 633

Thr His Ser Ser Val Ile Lys Leu Phe Asp Phe Ser Ser Asn Met Thr

20

25

30

tcc tta ttt ctg aac agt act ggt tac ttt caa aat gaa ttt tta ttg 681

Ser Leu Phe Leu Asn Ser Thr Gly Tyr Phe Gln Asn Glu Phe Leu Leu

35

40

45

aga ttt tcc att aac tat ttt ttt caa aga ctc aaa ttt tgt acc aag 729

Arg Phe Ser Ile Asn Tyr Phe Phe Gln Arg Leu Lys Phe Cys Thr Lys

50 55 60 65

taaatccagg ctttaatglac aaacaatgttg ttgtttttat ttggggctgg gggaggtata 789

tgatgagcag acttcicgga atlcataata aattttctaa aagcct 835

<210> 138

<211> 65

<212> PRT

<213> Homo sapiens

<400> 138

Met Ser Tyr Pro Phe Lys Gln Leu Leu Ala Ser Phe Lys Pro Lys Ile

1 5 10 15

Tyr Thr His Ser Ser Val Ile Lys Leu Phe Asp Phe Ser Ser Asn Met

20 25 30

Thr Ser Leu Phe Leu Asn Ser Thr Gly Tyr Phe Gln Asn Glu Phe Leu

35 40 45

Leu Arg Phe Ser Ile Asn Tyr Phe Phe Gln Arg Leu Lys Phe Cys Thr

50 55 60

Lys

65

<210> 139

<211> 626

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1).. (201)

<220>

<221> unsure

<222> (348)

<223> t or c

<220>

<221> unsure

<222> (353)

<223> a or t

<220>

<221> unsure

<222> (358)

<223> a or t

<220>

<221> unsure

<222> (363)

<223> a or t

<220>

<221> unsure

<222> (368)

<223> g or a

<400> 139

tgt ttc agt gtg act gtc ttg tta gag gtg aag ttt atc cag ggt aac 48

Cys Phe Ser Val Thr Val Leu Leu Glu Val Lys Phe Ile Gln Gly Asn

1

5

10

15

ttg ctc act aac tat tcc ttt tta tgg cct ggg gtt aaa ggg agc atg 96

Leu Leu Thr Asn Tyr Ser Phe Leu Trp Pro Gly Val Lys Gly Ser Met
 20 25 30
 gct cac act ggt gaa aat aag gaa ggc ctg gtc tta tct tgt att aat 144
 Ala His Thr Gly Glu Asn Lys Glu Gly Leu Val Leu Ser Cys Ile Asn
 35 40 45
 aat act ggc tgc att cca cca gcc aga gat ttc tat ctg cga aga cct 192
 Asn Thr Gly Cys Ile Pro Pro Ala Arg Asp Phe Tyr Leu Arg Arg Pro
 50 55 60
 atg aaa cac tgaagagaaa ttaggcaga aggaaatggc cacatacac 241
 Met Lys His
 65
 aagtictatt atatactctt ttglaaatac atattgtata ttacttggat gttttcttat 301
 atcatttact gtctttttga gttaatgtca gtttttactc tctcaaytta cwaatgwaca 361
 twgtaartaa cataaigtcc ttattatatt atatttaagc atctaacata tagagtigt 421
 ttcatataag tttaagataa atgtcaaaaa tatatgttct ttgtttttc ttgctttta 481
 aattatgtat cttttccttt tctttttttt aagaataatt tattgttcag gagaaagaat 541
 glatatgtaa ctgaaactat ctgaagaatg cacattgaag gccgtgaggt actgataaac 601
 taaagaattt attattcaaa atact 626

<210> 140

<211> 67

<212> PRT

<213> Homo sapiens

<400> 140

Cys Phe Ser Val Thr Val Leu Leu Glu Val Lys Phe Ile Gln Gly Asn
 1 5 10 15
 Leu Leu Thr Asn Tyr Ser Phe Leu Trp Pro Gly Val Lys Gly Ser Met

20 25 30
 Ala His Thr Gly Glu Asn Lys Glu Gly Leu Val Leu Ser Cys Ile Asn
 35 40 45
 Asn Thr Gly Cys Ile Pro Pro Ala Arg Asp Phe Tyr Leu Arg Arg Pro
 50 55 60
 Met Lys His

65

<210> 141

<211> 525

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (103).. (525)

<400> 141

aagaaatgga ggactcagaa ccaaggattt ccaagigatt tcttccaaag cacaggaatc 60
 tcactctgtt aaagctggtc tgttctaact gagatgacag tc atg tcc ctt tcc 114
 Met Ser Leu Ser

1

agg gac ctc aag gac gac ttt cac agt gac acg gta ctc tcc atc tta 162
 Arg Asp Leu Lys Asp Asp Phe His Ser Asp Thr Val Leu Ser Ile Leu
 5 10 15 20
 aat gag cag cgc att cgg ggc att tta tgc gat gtc act atc att gtg 210
 Asn Glu Gln Arg Ile Arg Gly Ile Leu Cys Asp Val Thr Ile Ile Val
 25 30 35
 gaa gat acc aaa ttt aaa gcc cat agc aat gtt ctg gca gct tca agc 258

Glu Asp Thr Lys Phe Lys Ala His Ser Asn Val Leu Ala Ala Ser Ser
 40 45 50
 ctg tat ttt aaa aat atc ttt tgg agc cat aca atc tgt att tcc agc 306
 Leu Tyr Phe Lys Asn Ile Phe Trp Ser His Thr Ile Cys Ile Ser Ser
 55 60 65
 cac gtc ctg gag ctg gac gat ctc aaa gct gaa gtg ttt act gaa ata 354
 His Val Leu Glu Leu Asp Asp Leu Lys Ala Glu Val Phe Thr Glu Ile
 70 75 80
 ctt aat tat atc tac agt tcc aca gtc gtt gtc aag aga cag gaa aca 402
 Leu Asn Tyr Ile Tyr Ser Ser Thr Val Val Val Lys Arg Gln Glu Thr
 85 90 95 100
 gtc act gat ctc gca gct gca gga aaa aag ctg gga ata tcg ttc ttg 450
 Val Thr Asp Leu Ala Ala Ala Gly Lys Lys Leu Gly Ile Ser Phe Leu
 105 110 115
 gaa gac ctt act gat cgc aac ttc tca aat tcc ccg ggt ccc tat gta 498
 Glu Asp Leu Thr Asp Arg Asn Phe Ser Asn Ser Pro Gly Pro Tyr Val
 120 125 130
 ttc tgt att act gaa aag gga gtg gtt 525
 Phe Cys Ile Thr Glu Lys Gly Val Val
 135 140

<210> 142

<211> 141

<212> PRT

<213> Homo sapiens

<400> 142

Met Ser Leu Ser Arg Asp Leu Lys Asp Asp Phe His Ser Asp Thr Val

1 5 10 15
Leu Ser Ile Leu Asn Glu Gln Arg Ile Arg Gly Ile Leu Cys Asp Val
20 25 30
Thr Ile Ile Val Glu Asp Thr Lys Phe Lys Ala His Ser Asn Val Leu
35 40 45
Ala Ala Ser Ser Leu Tyr Phe Lys Asn Ile Phe Trp Ser His Thr Ile
50 55 60
Cys Ile Ser Ser His Val Leu Glu Leu Asp Asp Leu Lys Ala Glu Val
65 70 75 80
Phe Thr Glu Ile Leu Asn Tyr Ile Tyr Ser Ser Thr Val Val Val Lys
85 90 95
Arg Gln Glu Thr Val Thr Asp Leu Ala Ala Ala Gly Lys Lys Leu Gly
100 105 110
Ile Ser Phe Leu Glu Asp Leu Thr Asp Arg Asn Phe Ser Asn Ser Pro
115 120 125
Gly Pro Tyr Val Phe Cys Ile Thr Glu Lys Gly Val Val
130 135 140

<210> 143

<211> 1827

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (138).. (1307)

<400> 143

gagacttggg ctggagccgc cctgggtgtc agcggctcgg ctcccgcgca cgctccggcc 60

gtgcgcagc ctccggcacct gcaggaccgt gcgtcccgcg gctggcgccc ctgactccgt 120
 cccggccagg gagggcc atg att tcc ctc ccg ggg ccc ctg gtg acc aac 170
 Met Ile Ser Leu Pro Gly Pro Leu Val Thr Asn
 1 5 10
 ttg ctg cgg ttt ttg ttc ctg ggg ctg agt gcc ctc gcg ccc ccc tcg 218
 Leu Leu Arg Phe Leu Phe Leu Gly Leu Ser Ala Leu Ala Pro Pro Ser
 15 20 25
 cgg gcc cag ctg caa ctg cac ttg ccc gcc aac cgg ttg cag gcg gtg 266
 Arg Ala Gln Leu Gln Leu His Leu Pro Ala Asn Arg Leu Gln Ala Val
 30 35 40
 gag gga ggg gaa gtg gtg ctt cca gcg tgg tac acc ttg cac ggg gag 314
 Glu Gly Gly Glu Val Val Leu Pro Ala Trp Tyr Thr Leu His Gly Glu
 45 50 55
 gtg tct tca tcc cag cca tgg gag gtg ccc ttt gtg atg tgg ttc ttc 362
 Val Ser Ser Ser Gln Pro Trp Glu Val Pro Phe Val Met Trp Phe Phe
 60 65 70 75
 aaa cag aaa gaa aag gag gat cag gtg ttg tcc tac atc aat ggg gtc 410
 Lys Gln Lys Glu Lys Glu Asp Gln Val Leu Ser Tyr Ile Asn Gly Val
 80 85 90
 aca aca agc aaa cct gga gta tcc ttg gtc tac tcc atg ccc tcc cgg 458
 Thr Thr Ser Lys Pro Gly Val Ser Leu Val Tyr Ser Met Pro Ser Arg
 95 100 105
 aac ctg tcc ctg cgg ctg gag ggt ctc cag gag aaa gac tct ggc ccc 506
 Asn Leu Ser Leu Arg Leu Glu Gly Leu Gln Glu Lys Asp Ser Gly Pro
 110 115 120
 tac agc tgc tcc gtg aat gtg caa gac aaa caa ggc aaa tct agg ggc 554
 Tyr Ser Cys Ser Val Asn Val Gln Asp Lys Gln Gly Lys Ser Arg Gly

125	130	135	
cac agc atc aaa acc tta gaa ctc aat gta ctg gtt cct cca gct cct	602		
His Ser Ile Lys Thr Leu Glu Leu Asn Val Leu Val Pro Pro Ala Pro			
140	145	150	155
cca tcc tgc cgt ctc cag ggt gtg ccc cat gtg ggg gca aac gtg acc	650		
Pro Ser Cys Arg Leu Gln Gly Val Pro His Val Gly Ala Asn Val Thr			
160	165	170	
ctg agc tgc cag tct cca agg agt aag cct gct gtc caa tac cag tgg	698		
Leu Ser Cys Gln Ser Pro Arg Ser Lys Pro Ala Val Gln Tyr Gln Trp			
175	180	185	
gat cgg cag ctt cca tcc ttc cag act ttc ttt gca cca gca tta gat	746		
Asp Arg Gln Leu Pro Ser Phe Gln Thr Phe Phe Ala Pro Ala Leu Asp			
190	195	200	
gtc atc cgt ggg tct tta agc ctc acc aac ctt tgc tct tcc atg gct	794		
Val Ile Arg Gly Ser Leu Ser Leu Thr Asn Leu Ser Ser Ser Met Ala			
205	210	215	
gga gtc tat gtc tgc aag gcc cac aat gag gtg ggc act gcc caa tgt	842		
Gly Val Tyr Val Cys Lys Ala His Asn Glu Val Gly Thr Ala Gln Cys			
220	225	230	235
aat gtg acg ctg gaa gtg agc aca ggg cct gga gct gca gtg gtt gct	890		
Asn Val Thr Leu Glu Val Ser Thr Gly Pro Gly Ala Ala Val Val Ala			
240	245	250	
gga gct gtt gtg ggt acc ctg gtt gga ctg ggg ttg ctg gct ggg ctg	938		
Gly Ala Val Val Gly Thr Leu Val Gly Leu Gly Leu Leu Ala Gly Leu			
255	260	265	
gtc ctc ttg tac cac cgc cgg ggc aag gcc ctg gag gag cca gcc aat	986		

Val Leu Leu Tyr His Arg Arg Gly Lys Ala Leu Glu Glu Pro Ala Asn
270 275 280
gat atc aag gag gat gcc att gct ccc cgg acc ctg ccc tgg ccc aag 1034
Asp Ile Lys Glu Asp Ala Ile Ala Pro Arg Thr Leu Pro Trp Pro Lys
285 290 295
agc tca gac aca atc tcc aag aat ggg acc ctt tcc tct gtc acc tcc 1082
Ser Ser Asp Thr Ile Ser Lys Asn Gly Thr Leu Ser Ser Val Thr Ser
300 305 310 315
gca cga gcc ctc tgg cca ccc cat ggc cct ccc agg cct ggt gca ttg 1130
Ala Arg Ala Leu Trp Pro Pro His Gly Pro Pro Arg Pro Gly Ala Leu
320 325 330
acc ccc acg ccc agt ctc tcc agc cag gcc ctg ccc tca cca aga ctg 1178
Thr Pro Thr Pro Ser Leu Ser Ser Gln Ala Leu Pro Ser Pro Arg Leu
335 340 345
ccc acg aca gat ggg gcc cac cct caa cca ata tcc ccc atc cct ggt 1226
Pro Thr Thr Asp Gly Ala His Pro Gln Pro Ile Ser Pro Ile Pro Gly
350 355 360
ggg gtt tct tcc tct ggc ttg agc cgc atg ggt gct gtg cct gtg atg 1274
Gly Val Ser Ser Ser Gly Leu Ser Arg Met Gly Ala Val Pro Val Met
365 370 375
gtg cct gcc cag agt caa gct ggc tct ctg gta tgatgacccc accactcatt 1327
Val Pro Ala Gln Ser Gln Ala Gly Ser Leu Val
380 385 390
ggctaaagga ttgggggtct ctcttcccta taagggtcac ctctagcaca gaggcctgag 1387
tcatgggaaa gagtcacact cctgaccctt agtactctgc cccaccctct ctttactgtg 1447
ggaaaaccaa ctcagtaaga cctaagtgtc caggagacag aaggagaaga ggaagtggat 1507
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<400> 144

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Val Leu Pro Ala Trp Tyr Thr Leu His Gly Glu Val Ser Ser Ser Gln

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Pro Trp Glu Val Pro Phe Val Met Trp Phe Phe Lys Gln Lys Glu Lys

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Glu Asp Gln Val Leu Ser Tyr Ile Asn Gly Val Thr Thr Ser Lys Pro

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Gly Val Ser Leu Val Tyr Ser Met Pro Ser Arg Asn Leu Ser Leu Arg

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Leu Glu Gly Leu Gln Glu Lys Asp Ser Gly Pro Tyr Ser Cys Ser Val

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Asn Val Gln Asp Lys Gln Gly Lys Ser Arg Gly His Ser Ile Lys Thr
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Gln Gly Val Pro His Val Gly Ala Asn Val Thr Leu Ser Cys Gln Ser
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Pro Arg Ser Lys Pro Ala Val Gln Tyr Gln Trp Asp Arg Gln Leu Pro
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Lys Ala His Asn Glu Val Gly Thr Ala Gln Cys Asn Val Thr Leu Glu
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Ser Lys Asn Gly Thr Leu Ser Ser Val Thr Ser Ala Arg Ala Leu Trp
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340

345

350

Ala His Pro Gln Pro Ile Ser Pro Ile Pro Gly Gly Val Ser Ser Ser

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Met Lys Lys Gln Phe Asn Arg Met Lys Gln

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Leu Ala Asn Gln Thr Val Gly Arg Ala Glu Lys Thr Glu Val Leu Ser

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25

gaa gat cta tta cag att gag aga cgc ctg gac acg gtg cgg tca ata 209

Glu Asp Leu Leu Gln Ile Glu Arg Arg Leu Asp Thr Val Arg Ser Ile

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35

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Cys His His Ser His Lys Arg Leu Val Ala Cys Phe Gln Gly Gln His	
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Gly Thr Asp Ala Glu Arg Arg His Lys Lys Leu Pro Leu Thr Ala Leu	
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Gly Lys Met Leu Glu Thr Cys Gly Asp Ala Glu Asn Gln Leu Ala Leu	
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Glu Leu Ser Gln His Glu Val Phe Val Glu Lys Glu Ile Val Asp Pro	
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Lys Gln Leu Ala Arg Leu Val Leu Asp Trp Asp Ser Val Arg Ala Arg	
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Ser Lys Ile Asp Thr Leu Lys Glu Glu Met Asp Glu Ala Gly Asn Lys	
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Arg Asn Glu Gly Thr Leu Ala Glu Met Ala Ala Ala Thr Ser Val His				
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Val Val Ala Val Ile Glu Pro Ile Ile Gln His Ala Asp Trp Phe Phe				
430	435	440		
cct gaa gag gtg gaa ttt aat gta tca gaa gca ttt gta cct ctc acc	1457			
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cca ggc gac ggc agt cct ccc aaa ccg aag gac cct gla tct gca gct	1841		
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 Ser Pro Lys Pro Pro Thr Arg Ser Pro Ser Pro Pro Thr Gln His Thr
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<212> PRT

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50 55 60

Arg His Lys Lys Leu Pro Leu Thr Ala Leu Ala Gln Asn Met Gln Glu

466/527

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 Pro Gln Asn Phe Val Asn Phe Arg Tyr Leu Ile Lys Phe Leu Ala Lys
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 485 490 495

Ser Phe Gly Val Lys Leu Met Asp Phe Gln Ala His Arg Arg Gly Gly
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Ser Pro Arg Ala Leu Thr Gln Pro Leu Gly Leu Leu Arg Leu Leu Gln
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Tyr Val Gln Phe Leu Ser His Gly Arg Ser Arg Asp His Ala Ile Ala			
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<211> 322

<212> PRT

<213> Homo sapiens

<400> 148

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Thr Gln Pro Leu Gly Leu Leu Arg Leu Leu Gln Leu Val Ser Thr Cys

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Val Ala Phe Ser Leu Val Ala Ser Val Gly Ala Trp Thr Gly Ser Met

50 55 60

Gly Asn Trp Ser Met Phe Thr Trp Cys Phe Cys Phe Ser Val Thr Leu

65 70 75 80

Ile Ile Leu Ile Val Glu Leu Cys Gly Leu Gln Ala Arg Phe Pro Leu

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Ser Trp Arg Asn Phe Pro Ile Thr Phe Ala Cys Tyr Ala Gly Leu Phe

100 105 110

Cys Leu Ser Ala Ser Ile Ile Tyr Pro Thr Thr Tyr Val Gln Phe Leu

115 120 125

Ser His Gly Arg Ser Arg Asp His Ala Ile Ala Ala Thr Phe Phe Ser

130 135 140

Cys Ile Ala Cys Val Ala Tyr Ala Thr Glu Val Ala Trp Thr Arg Ala

145 150 155 160

Arg Pro Gly Glu Ile Thr Gly Tyr Met Ala Thr Val Pro Gly Leu Leu

165 170 175

Lys Val Leu Glu Thr Phe Val Ala Cys Ile Ile Phe Ala Phe Ile Ser

180 185 190

Asp Pro Asn Leu Tyr Gln His Gln Pro Ala Leu Glu Trp Cys Val Ala

195 200 205

Val Tyr Ala Ile Cys Phe Ile Leu Ala Ala Ile Ala Ile Leu Leu Asn

210 215 220

Leu Gly Glu Cys Thr Asn Val Leu Pro Ile Pro Phe Pro Ser Phe Leu

225 230 235 240

Ser Gly Leu Ala Leu Leu Ser Val Leu Leu Tyr Ala Thr Ala Leu Val

245 250 255

Leu Trp Pro Leu Tyr Gln Phe Asp Glu Lys Tyr Gly Gly Gln Pro Arg

260 265 270

Arg Ser Arg Asp Val Ser Cys Ser Arg Ser His Ala Tyr Tyr Val Cys

275 280 285

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Lys Val

<210> 149

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<400> 149

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 Ser Gln Gly Val Val Leu Thr Ala Tyr His Pro Ser Gly Lys Asp Gln
 10 15 20
 gcc gtc ggg aac agc cat gca aag gca ggg gag gaa gcc acc tcg agt 152
 Ala Val Gly Asn Ser His Ala Lys Ala Gly Glu Glu Ala Thr Ser Ser
 25 30 35
 cgc aga tat ggc cag tac act atg aac cag gaa agc acc acc atc aaa 200
 Arg Arg Tyr Gly Gln Tyr Thr Met Asn Gln Glu Ser Thr Thr Ile Lys
 40 45 50
 gtt atg gag aag cct cca ttt gat cga tca att tcc cag gat tct ttg 248
 Val Met Glu Lys Pro Pro Phe Asp Arg Ser Ile Ser Gln Asp Ser Leu
 55 60 65 70
 gat gaa cta tct atg gaa gac tat tgg ata gaa cta gaa aac atc aag 296
 Asp Glu Leu Ser Met Glu Asp Tyr Trp Ile Glu Leu Glu Asn Ile Lys
 75 80 85
 aaa tct agt gaa aac agc caa gaa gat caa gag gtg gtt gtt gtc aaa 344
 Lys Ser Ser Glu Asn Ser Gln Glu Asp Gln Glu Val Val Val Val Lys
 90 95 100
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 Glu Pro Asp Glu Gly Glu Leu Glu Glu Glu Trp Leu Lys Glu Ala Gly
 105 110 115
 tta tcc aat ctc ttc gga gag tct gct gga gat cca cag gaa agc att 440
 Leu Ser Asn Leu Phe Gly Glu Ser Ala Gly Asp Pro Gln Glu Ser Ile
 120 125 130
 gtg ttt tta tca aca ttg acg cgg acc cag gca gca gca gtt cag aag 488
 Val Phe Leu Ser Thr Leu Thr Arg Thr Gln Ala Ala Ala Val Gln Lys

135	140	145	150	
cga gta gag acg gtc tcc cag acc ttg agg aaa aaa aac aaa cag tac	536			
Arg Val Glu Thr Val Ser Gln Thr Leu Arg Lys Lys Asn Lys Gln Tyr				
155	160	165		
cag att cct gac gtc aga gac ata ttt gct caa cag aga gaa tca aaa	584			
Gln Ile Pro Asp Val Arg Asp Ile Phe Ala Gln Gln Arg Glu Ser Lys				
170	175	180		
gaa aca gct cca ggt ggc act gaa tgc cag tca ctt aga aca aat gaa	632			
Glu Thr Ala Pro Gly Gly Thr Glu Ser Gln Ser Leu Arg Thr Asn Glu				
185	190	195		
aac aaa tac caa gga aga gat gac gag gca tct aac ctt gtt ggt gaa	680			
Asn Lys Tyr Gln Gly Arg Asp Asp Glu Ala Ser Asn Leu Val Gly Glu				
200	205	210		
gag aag ctg atc cca cct gag gag acg cct gcc cct gaa aca gac atc	728			
Glu Lys Leu Ile Pro Pro Glu Glu Thr Pro Ala Pro Glu Thr Asp Ile				
215	220	225	230	
aac ctg gag gta tca ttt gcc gag caa gca ctc aat cag aaa gag agc	776			
Asn Leu Glu Val Ser Phe Ala Glu Gln Ala Leu Asn Gln Lys Glu Ser				
235	240	245		
tcc aag gag aaa atc cag aag agc aaa ggc gat gat gcc aca tta cct	824			
Ser Lys Glu Lys Ile Gln Lys Ser Lys Gly Asp Asp Ala Thr Leu Pro				
250	255	260		
agt ttc aga ttg cca aaa gac aaa acg ggt acc aca agg att ggt gac	872			
Ser Phe Arg Leu Pro Lys Asp Lys Thr Gly Thr Thr Arg Ile Gly Asp				
265	270	275		
ctc gca ccc cag gac atg aag aaa gtt tgc cat tta gcc cta att gag	920			
Leu Ala Pro Gln Asp Met Lys Lys Val Cys His Leu Ala Leu Ile Glu				

280	285	290	
ctg act gcc ctc tat gal gta ttg ggt att gag ctg aaa caa caa aaa	968		
Leu Thr Ala Leu Tyr Asp Val Leu Gly Ile Glu Leu Lys Gln Gln Lys			
295	300	305	310
gct gtg aaa atc aaa aca aaa gat tct ggt ctt ttt tgc gtt cca ttg	1016		
Ala Val Lys Ile Lys Thr Lys Asp Ser Gly Leu Phe Cys Val Pro Leu			
315	320	325	
aca gcg cta tta gaa caa gat cag agg aaa gta cca gga atg cga ata	1064		
Thr Ala Leu Leu Glu Gln Asp Gln Arg Lys Val Pro Gly Met Arg Ile			
330	335	340	
ccc ttg atc ttt caa aaa ctg att tct cga att gaa gag aga ggt ttg	1112		
Pro Leu Ile Phe Gln Lys Leu Ile Ser Arg Ile Glu Glu Arg Gly Leu			
345	350	355	
gaa aca gaa ggc ctc tta cgg atc cct gga gct gcc att aga atc aag	1160		
Glu Thr Glu Gly Leu Leu Arg Ile Pro Gly Ala Ala Ile Arg Ile Lys			
360	365	370	
aat ctt tgc caa gaa cta gaa gca aag ttt tat gaa ggg act ttt aat	1208		
Asn Leu Cys Gln Glu Leu Glu Ala Lys Phe Tyr Glu Gly Thr Phe Asn			
375	380	385	390
tgg gaa agt gtc aaa cag cat gat gcc gcc agc ctg ctg aag ctc ttc	1256		
Trp Glu Ser Val Lys Gln His Asp Ala Ala Ser Leu Leu Lys Leu Phe			
395	400	405	
att cgg gag ttg ccc cag cca ctg ctc agt gtg gag tat ctc aaa gcc	1304		
Ile Arg Glu Leu Pro Gln Pro Leu Leu Ser Val Glu Tyr Leu Lys Ala			
410	415	420	
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Phe Gln Ala Val Gln Asn Leu Pro Thr Lys Lys Gln Gln Leu Gln Ala
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 440 445 450
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 Lys Ala Leu Leu Glu Phe Leu Gln Arg Val Ile Asp Asn Lys Glu Lys
 455 460 465 470
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 Asn Lys Met Thr Val Met Asn Val Ala Met Val Met Ala Pro Asn Leu
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 Phe Met Cys His Ala Leu Gly Leu Lys Ser Ser Glu Gln Arg Glu Phe
 490 495 500
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 Val Met Ala Ala Gly Thr Ala Asn Thr Met His Leu Leu Ile Lys Tyr
 505 510 515
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 520 525 530
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 Lys Gln Asn Thr Glu Asn His Lys Lys Asp Lys Arg Ala Met Lys Lys
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 Ala Pro His Leu Ser Lys Val Ser Met Ala Ile Gln Leu Thr Glu Glu
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 Gly Asn Ile Gly Glu Arg Cys Leu Asp Asp Asp Thr Tyr Met Lys Asp
 635 640 645
 tta tat cag ctt aac cca aat gct gag tgg gtt ata aag tca aag cca 2024
 Leu Tyr Gln Leu Asn Pro Asn Ala Glu Trp Val Ile Lys Ser Lys Pro
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<211> 663

<212> PRT

<213> Homo sapiens

<400> 150

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Glu Glu Ala Thr Ser Ser Arg Arg Tyr Gly Gln Tyr Thr Met Asn Gln

35 40 45

Glu Ser Thr Thr Ile Lys Val Met Glu Lys Pro Pro Phe Asp Arg Ser

50 55 60

Ile Ser Gln Asp Ser Leu Asp Glu Leu Ser Met Glu Asp Tyr Trp Ile

65 70 75 80

Glu Leu Glu Asn Ile Lys Lys Ser Ser Glu Asn Ser Gln Glu Asp Gln

85 90 95

Glu Val Val Val Val Lys Glu Pro Asp Glu Gly Glu Leu Glu Glu Glu

100 105 110

Trp Leu Lys Glu Ala Gly Leu Ser Asn Leu Phe Gly Glu Ser Ala Gly

115 120 125

WO 01/25427

Asp Pro Gln Glu Ser Ile Val Phe Leu Ser Thr Leu Thr Arg Thr Gln
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 Ala Ala Ala Val Gln Lys Arg Val Glu Thr Val Ser Gln Thr Leu Arg
 145 150 155 160
 Lys Lys Asn Lys Gln Tyr Gln Ile Pro Asp Val Arg Asp Ile Phe Ala
 165 170 175
 Gln Gln Arg Glu Ser Lys Glu Thr Ala Pro Gly Gly Thr Glu Ser Gln
 180 185 190
 Ser Leu Arg Thr Asn Glu Asn Lys Tyr Gln Gly Arg Asp Asp Glu Ala
 195 200 205
 Ser Asn Leu Val Gly Glu Glu Lys Leu Ile Pro Pro Glu Glu Thr Pro
 210 215 220
 Ala Pro Glu Thr Asp Ile Asn Leu Glu Val Ser Phe Ala Glu Gln Ala
 225 230 235 240
 Leu Asn Gln Lys Glu Ser Ser Lys Glu Lys Ile Gln Lys Ser Lys Gly
 245 250 255
 Asp Asp Ala Thr Leu Pro Ser Phe Arg Leu Pro Lys Asp Lys Thr Gly
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 Thr Thr Arg Ile Gly Asp Leu Ala Pro Gln Asp Met Lys Lys Val Cys
 275 280 285
 His Leu Ala Leu Ile Glu Leu Thr Ala Leu Tyr Asp Val Leu Gly Ile
 290 295 300
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 305 310 315 320
 Leu Phe Cys Val Pro Leu Thr Ala Leu Leu Glu Gln Asp Gln Arg Lys
 325 330 335

Val Pro Gly Met Arg Ile Pro Leu Ile Phe Gln Lys Leu Ile Ser Arg
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Ile Glu Glu Arg Gly Leu Glu Thr Glu Gly Leu Leu Arg Ile Pro Gly
355 360 365
Ala Ala Ile Arg Ile Lys Asn Leu Cys Gln Glu Leu Glu Ala Lys Phe
370 375 380
Tyr Glu Gly Thr Phe Asn Trp Glu Ser Val Lys Gln His Asp Ala Ala
385 390 395 400
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Lys Gln Gln Leu Gln Ala Leu Asn Leu Leu Gly Ile Leu Leu Pro Asp
435 440 445
Ala Asn Arg Asp Thr Leu Lys Ala Leu Leu Glu Phe Leu Gln Arg Val
450 455 460
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465 470 475 480
Val Met Ala Pro Asn Leu Phe Met Cys His Ala Leu Gly Leu Lys Ser
485 490 495
Ser Glu Gln Arg Glu Phe Val Met Ala Ala Gly Thr Ala Asn Thr Met
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His Leu Leu Ile Lys Tyr Gln Lys Leu Leu Trp Thr Ile Pro Lys Phe
515 520 525
Ile Val Asn Gln Val Arg Lys Gln Asn Thr Glu Asn His Lys Lys Asp
530 535 540
Lys Arg Ala Met Lys Lys Leu Leu Lys Lys Met Ala Tyr Asp Arg Glu

545 550 555 560
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 565 570 575
 Gly Val Ile Arg Val Gln Ala Pro His Leu Ser Lys Val Ser Met Ala
 580 585 590
 Ile Gln Leu Thr Glu Glu Leu Lys Ala Ser Asp Val Leu Ala Arg Phe
 595 600 605
 Leu Ser Gln Glu Ser Gly Val Ala Gln Thr Leu Lys Lys Gly Glu Val
 610 615 620
 Phe Leu Tyr Glu Ile Gly Gly Asn Ile Gly Glu Arg Cys Leu Asp Asp
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<212> DNA

<213> Homo sapiens

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<221> CDS

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15

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 cca gac gag gta gcc aag gag ctg gag ctg ctc ggg gga tgg aca gat 143
 Pro Asp Glu Val Ala Lys Glu Leu Glu Leu Leu Gly Gly Trp Thr Asp
 35 40 45
 gac aaa aaa gta cca ggc aga atg tac agt aat aac cct ttc tgg aat 191
 Asp Lys Lys Val Pro Gly Arg Met Tyr Ser Asn Asn Pro Phe Trp Asn
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 ggg gtc cag acc aat cca ttt ctg aat ggg aac gtg ccc gtc atg ccc 239
 Gly Val Gln Thr Asn Pro Phe Leu Asn Gly Asn Val Pro Val Met Pro
 65 70 75
 agc ctg gat gag ctg aat ccc aaa agt act gtg gat ttg ctc ctt ttt 287
 Ser Leu Asp Glu Leu Asn Pro Lys Ser Thr Val Asp Leu Leu Leu Phe
 80 85 90 95
 gac gca ggt aca tcc tcc ttc acc gaa tcc agc tca gcc acc acg aat 335
 Asp Ala Gly Thr Ser Ser Phe Thr Glu Ser Ser Ser Ala Thr Thr Asn
 100 105 110
 agc act ggc aac atc ttc gat gag ctt cca gtc aca aac ggg ctc cac 383
 Ser Thr Gly Asn Ile Phe Asp Glu Leu Pro Val Thr Asn Gly Leu His
 115 120 125
 gca gag ccg ccg gtc agg cgg gac aac ccc ttc ttc aga agc aag cgc 431
 Ala Glu Pro Pro Val Arg Arg Asp Asn Pro Phe Phe Arg Ser Lys Arg
 130 135 140
 tcc tac agt ctc tcg gaa ctc tcc gtc ctc caa gcc aag tcc gac gct 479
 Ser Tyr Ser Leu Ser Glu Leu Ser Val Leu Gln Ala Lys Ser Asp Ala

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Pro Thr Ser Ser Ser Phe Phe Thr Gly Leu Lys Ser Pro Ala Pro Glu			
160	165	170	175
caa ttt cag agc cgg gag gat ttt cga act gcc tgg cta aac cac agg	575		
Gln Phe Gln Ser Arg Glu Asp Phe Arg Thr Ala Trp Leu Asn His Arg			
180	185	190	
aag ctg gcc cgg tct tgc cac gac ctg gac ttg ctt ggc caa agc cct	623		
Lys Leu Ala Arg Ser Cys His Asp Leu Asp Leu Leu Gly Gln Ser Pro			
195	200	205	
ggc tgg ggc cag acc caa gcc gtg gag aca aac atc gtg tgc aag ctg	671		
Gly Trp Gly Gln Thr Gln Ala Val Glu Thr Asn Ile Val Cys Lys Leu			
210	215	220	
gat agc tcc ggg ggt gct gtc cag ctt cct gac acc agc atc agc atc	719		
Asp Ser Ser Gly Gly Ala Val Gln Leu Pro Asp Thr Ser Ile Ser Ile			
225	230	235	
cac gtg ccc gag ggc cac gtc gcc cct ggg gag acc cag cag atc tcc	767		
His Val Pro Glu Gly His Val Ala Pro Gly Glu Thr Gln Gln Ile Ser			
240	245	250	255
atg aaa gcc ctg ctg gac ccc ccg ctg gag ctc aac agt gac agg tcc	815		
Met Lys Ala Leu Leu Asp Pro Pro Leu Glu Leu Asn Ser Asp Arg Ser			
260	265	270	
tgc agc atc agc cct gtg ctg gag gtc aag ctg agc aac ctg gag gtg	863		
Cys Ser Ile Ser Pro Val Leu Glu Val Lys Leu Ser Asn Leu Glu Val			
275	280	285	
aaa acc tct atc atc ttg gag atg aaa gtg tca gcc gag ata aaa aat	911		
Lys Thr Ser Ile Ile Leu Glu Met Lys Val Ser Ala Glu Ile Lys Asn			

290	295	300	
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Asp Leu Phe Ser Lys Ser Thr Val Gly Leu Gln Cys Leu Arg Ser Asp			
305	310	315	
tcg aag gaa ggg cca tat gtc tcc gtc ccg ctc aac tgc agc tgt ggg			1007
Ser Lys Glu Gly Pro Tyr Val Ser Val Pro Leu Asn Cys Ser Cys Gly			
320	325	330	335
gac acg gtc cag gca cag ctg cac aac ctg gag ccc tgt atg tac gtg			1055
Asp Thr Val Gln Ala Gln Leu His Asn Leu Glu Pro Cys Met Tyr Val			
340	345	350	
gct gtc gtg gcc cat ggc cca agc atc ctc tac cct tcc acc gtg tgg			1103
Ala Val Val Ala His Gly Pro Ser Ile Leu Tyr Pro Ser Thr Val Trp			
355	360	365	
gac ttc atc aat aaa aaa gtc aca gtg ggt ctc tac ggc cct aaa cac			1151
Asp Phe Ile Asn Lys Lys Val Thr Val Gly Leu Tyr Gly Pro Lys His			
370	375	380	
atc cac cca tcc ttc aag acg gla gtg acc att ttt ggg cat gac tgt			1199
Ile His Pro Ser Phe Lys Thr Val Val Thr Ile Phe Gly His Asp Cys			
385	390	395	
gcc cca aag acg ctc ctg gtc agc gag gtc aca cgc cag gca ccc aac			1247
Ala Pro Lys Thr Leu Leu Val Ser Glu Val Thr Arg Gln Ala Pro Asn			
400	405	410	415
cct gcc ccg gtg gcc ctg cag ctg tgg ggg aag cac cag ttc gtt ttg			1295
Pro Ala Pro Val Ala Leu Gln Leu Trp Gly Lys His Gln Phe Val Leu			
420	425	430	
tcc agg ccc cag gat ctc aag gtc tgt atg ttt tcc aat atg acg aat			1343

Ser Arg Pro Gln Asp Leu Lys Val Cys Met Phe Ser Asn Met Thr Asn
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 Tyr Glu Val Lys Ala Ser Glu Gln Ala Lys Val Val Arg Gly Phe Gln
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 Asn Pro Asn Glu Leu Ser Asp Phe Thr Leu Arg Val Gln Val Lys Asp
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 Asp Gln Glu Ala Ile Leu Thr Gln Phe Cys Val Gln Thr Pro Gln Pro
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 Pro Pro Lys Ser Ala Ile Lys Pro Ser Gly Gln Arg Arg Phe Leu Lys
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 Lys Asn Glu Val Gly Lys Ile Ile Leu Ser Pro Phe Ala Thr Thr Thr
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 Lys Tyr Pro Thr Phe Gln Asp Arg Pro Val Ser Ser Leu Lys Phe Gly
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 Lys Leu Leu Lys Thr Val Val Arg Gln Asn Lys Asn His Tyr Leu Leu
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 gag tac aag aag ggc gac ggg atc gcc ctg ctc agc gag gag cgg gtc 1775

Glu Tyr Lys Lys Gly Asp Gly Ile Ala Leu Leu Ser Glu Glu Arg Val
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 Arg Leu Arg Gly Gln Leu Trp Thr Lys Glu Trp Tyr Ile Gly Tyr Tyr
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 Gln Gly Arg Val Gly Leu Val His Thr Lys Asn Val Leu Val Val Gly
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 675 680 685
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 Lys Leu Lys Glu Asp Cys Asn Asn Thr Glu Asn Lys Glu Arg Lys Ser
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 Phe Gln Lys Glu Leu Val Met Ala Leu Leu Lys Met Asp Cys Gln Gly
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 Glu Val Ala Gln Arg Trp Arg Glu Leu Ala Glu Lys Leu Ala Lys Val
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 Gly Val Val Asp Ser Glu Ala Met Trp Lys Pro Ala Tyr Asp Phe Leu
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 gag ctg cac ctg ggc ctg gac aag atg aaa aac ccc atc acc aag cgc 2495
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 Trp Lys His Leu Thr Gly Thr Leu Ile Leu Val Asn Ser Leu Asp Val
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<211> 863

<212> PRT

<213> Homo sapiens

<400> 152

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35 40 45

Lys Lys Val Pro Gly Arg Met Tyr Ser Asn Asn Pro Phe Trp Asn Gly

50 55 60

Val Gln Thr Asn Pro Phe Leu Asn Gly Asn Val Pro Val Met Pro Ser

65 70 75 80

Leu Asp Glu Leu Asn Pro Lys Ser Thr Val Asp Leu Leu Leu Phe Asp

85 90 95

Ala Gly Thr Ser Ser Phe Thr Glu Ser Ser Ser Ala Thr Thr Asn Ser

100 105 110

Thr Gly Asn Ile Phe Asp Glu Leu Pro Val Thr Asn Gly Leu His Ala

115 120 125
Glu Pro Pro Val Arg Arg Asp Asn Pro Phe Phe Arg Ser Lys Arg Ser
130 135 140
Tyr Ser Leu Ser Glu Leu Ser Val Leu Gln Ala Lys Ser Asp Ala Pro
145 150 155 160
Thr Ser Ser Ser Phe Phe Thr Gly Leu Lys Ser Pro Ala Pro Glu Gln
165 170 175
Phe Gln Ser Arg Glu Asp Phe Arg Thr Ala Trp Leu Asn His Arg Lys
180 185 190
Leu Ala Arg Ser Cys His Asp Leu Asp Leu Leu Gly Gln Ser Pro Gly
195 200 205
Trp Gly Gln Thr Gln Ala Val Glu Thr Asn Ile Val Cys Lys Leu Asp
210 215 220
Ser Ser Gly Gly Ala Val Gln Leu Pro Asp Thr Ser Ile Ser Ile His
225 230 235 240
Val Pro Glu Gly His Val Ala Pro Gly Glu Thr Gln Gln Ile Ser Met
245 250 255
Lys Ala Leu Leu Asp Pro Pro Leu Glu Leu Asn Ser Asp Arg Ser Cys
260 265 270
Ser Ile Ser Pro Val Leu Glu Val Lys Leu Ser Asn Leu Glu Val Lys
275 280 285
Thr Ser Ile Ile Leu Glu Met Lys Val Ser Ala Glu Ile Lys Asn Asp
290 295 300
Leu Phe Ser Lys Ser Thr Val Gly Leu Gln Cys Leu Arg Ser Asp Ser
305 310 315 320
Lys Glu Gly Pro Tyr Val Ser Val Pro Leu Asn Cys Ser Cys Gly Asp
325 330 335

Thr Val Gln Ala Gln Leu His Asn Leu Glu Pro Cys Met Tyr Val Ala
340 345 350
Val Val Ala His Gly Pro Ser Ile Leu Tyr Pro Ser Thr Val Trp Asp
355 360 365
Phe Ile Asn Lys Lys Val Thr Val Gly Leu Tyr Gly Pro Lys His Ile
370 375 380
His Pro Ser Phe Lys Thr Val Val Thr Ile Phe Gly His Asp Cys Ala
385 390 395 400
Pro Lys Thr Leu Leu Val Ser Glu Val Thr Arg Gln Ala Pro Asn Pro
405 410 415
Ala Pro Val Ala Leu Gln Leu Trp Gly Lys His Gln Phe Val Leu Ser
420 425 430
Arg Pro Gln Asp Leu Lys Val Cys Met Phe Ser Asn Met Thr Asn Tyr
435 440 445
Glu Val Lys Ala Ser Glu Gln Ala Lys Val Val Arg Gly Phe Gln Leu
450 455 460
Lys Leu Gly Lys Val Ser Arg Leu Ile Phe Pro Ile Thr Ser Gln Asn
465 470 475 480
Pro Asn Glu Leu Ser Asp Phe Thr Leu Arg Val Gln Val Lys Asp Asp
485 490 495
Gln Glu Ala Ile Leu Thr Gln Phe Cys Val Gln Thr Pro Gln Pro Pro
500 505 510
Pro Lys Ser Ala Ile Lys Pro Ser Gly Gln Arg Arg Phe Leu Lys Lys
515 520 525
Asn Glu Val Gly Lys Ile Ile Leu Ser Pro Phe Ala Thr Thr Thr Lys
530 535 540

Tyr Pro Thr Phe Gln Asp Arg Pro Val Ser Ser Leu Lys Phe Gly Lys
 545 550 555 560
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 565 570 575
 Tyr Lys Lys Gly Asp Gly Ile Ala Leu Leu Ser Glu Glu Arg Val Arg
 580 585 590
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 595 600 605
 Gly Arg Val Gly Leu Val His Thr Lys Asn Val Leu Val Val Gly Arg
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 Ala Arg Pro Ser Leu Cys Ser Gly Pro Glu Leu Ser Thr Ser Val Leu
 625 630 635 640
 Leu Glu Gln Ile Leu Arg Pro Cys Lys Phe Leu Thr Tyr Ile Tyr Ala
 645 650 655
 Ser Val Arg Thr Leu Leu Met Glu Asn Ile Ser Ser Trp Arg Ser Phe
 660 665 670
 Ala Asp Ala Leu Gly Tyr Val Asn Leu Pro Leu Thr Phe Phe Cys Arg
 675 680 685
 Ala Glu Leu Asp Ser Glu Pro Glu Arg Val Ala Ser Val Leu Glu Lys
 690 695 700
 Leu Lys Glu Asp Cys Asn Asn Thr Glu Asn Lys Glu Arg Lys Ser Phe
 705 710 715 720
 Gln Lys Glu Leu Val Met Ala Leu Leu Lys Met Asp Cys Gln Gly Leu
 725 730 735
 Val Val Arg Leu Ile Gln Asp Phe Val Leu Leu Thr Thr Ala Val Glu
 740 745 750
 Val Ala Gln Arg Trp Arg Glu Leu Ala Glu Lys Leu Ala Lys Val Ser

755	760	765	
Lys Gln Gln Met Asp Ala Tyr Glu Ser Pro His Arg Asp Arg Asn Gly			
770	775	780	
Val Val Asp Ser Glu Ala Met Trp Lys Pro Ala Tyr Asp Phe Leu Leu			
785	790	795	800
Thr Trp Ser His Gln Ile Gly Asp Ser Tyr Arg Asp Val Ile Gln Glu			
	805	810	815
Leu His Leu Gly Leu Asp Lys Met Lys Asn Pro Ile Thr Lys Arg Trp			
	820	825	830
Lys His Leu Thr Gly Thr Leu Ile Leu Val Asn Ser Leu Asp Val Leu			
	835	840	845
Arg Ala Ala Ala Phe Ser Pro Ala Asp Gln Asp Asp Phe Val Ile			
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<210> 153

<211> 2194

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

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<400> 153

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gcggggcgccg gc atg tgg ctg tgg gag gac cag ggc ggc ctg ctg ggc cct 171

Met Trp Leu Trp Glu Asp Gln Gly Gly Leu Leu Gly Pro

1

5

10

ttc tcc ttc ctg ctg cta gtg ctg ctg ctg gtg acg cgg agc ccg gtc 219
 Phe Ser Phe Leu Leu Leu Val Leu Leu Leu Val Thr Arg Ser Pro Val
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 aat gcc tgc ctc ctc acc ggc agc ctc ttc gtt cta ctg cgc gtc ttc 267
 Asn Ala Cys Leu Leu Thr Gly Ser Leu Phe Val Leu Leu Arg Val Phe
 30 35 40 45
 agc ttt gag ccg gtg ccc tct tgc agg gcc ctg cag gtg ctc aag ccc 315
 Ser Phe Glu Pro Val Pro Ser Cys Arg Ala Leu Gln Val Leu Lys Pro
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 cgg gac cgc att tct gcc atc gcc cac cgt ggc ggc agc cac gac gcg 363
 Arg Asp Arg Ile Ser Ala Ile Ala His Arg Gly Gly Ser His Asp Ala
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 ccc gag aac acg ctg gcg gcc att cgg cag gca gct aag aat gga gca 411
 Pro Glu Asn Thr Leu Ala Ala Ile Arg Gln Ala Ala Lys Asn Gly Ala
 80 85 90
 aca ggc gtg gag ttg gac att gag ttt act tct gac ggg att cct gtc 459
 Thr Gly Val Glu Leu Asp Ile Glu Phe Thr Ser Asp Gly Ile Pro Val
 95 100 105
 tta atg cac gat aac aca gla gat agg acg act gat ggg act ggg cga 507
 Leu Met His Asp Asn Thr Val Asp Arg Thr Thr Asp Gly Thr Gly Arg
 110 115 120 125
 ttg tgt gat ttg aca ttt gaa caa att agg aag ctg aat cct gca gca 555
 Leu Cys Asp Leu Thr Phe Glu Gln Ile Arg Lys Leu Asn Pro Ala Ala
 130 135 140
 aac cac aga ctc agg aat gat ttc cct gat gaa aag atc cct acc cta 603
 Asn His Arg Leu Arg Asn Asp Phe Pro Asp Glu Lys Ile Pro Thr Leu

145	150	155	
agg gaa gct gtt gca gag tgc cta aac cat aac ctc aca atc ttc ttt			651
Arg Glu Ala Val Ala Glu Cys Leu Asn His Asn Leu Thr Ile Phe Phe			
160	165	170	
gat gtc aaa ggc cat gca cac aag gct act gag gct cta aag aaa atg			699
Asp Val Lys Gly His Ala His Lys Ala Thr Glu Ala Leu Lys Lys Met			
175	180	185	
tat atg gaa ttt cct caa ctg tat aat aat agt gtg gtc tgt tct ttc			747
Tyr Met Glu Phe Pro Gln Leu Tyr Asn Asn Ser Val Val Cys Ser Phe			
190	195	200	205
ttg cca gaa gtt atc tac aag atg aga caa aca gat cgg gat gta ata			795
Leu Pro Glu Val Ile Tyr Lys Met Arg Gln Thr Asp Arg Asp Val Ile			
210	215	220	
aca gca tta act cac aga cct tgg agc cta agc cat aca gga gat ggg			843
Thr Ala Leu Thr His Arg Pro Trp Ser Leu Ser His Thr Gly Asp Gly			
225	230	235	
aaa cca cgc tat gat act ttc tgg aaa cat ttt ata ttt gtt atg atg			891
Lys Pro Arg Tyr Asp Thr Phe Trp Lys His Phe Ile Phe Val Met Met			
240	245	250	
gac att ttg ctc gat tgg agc atg cat aat atc ttg tgg tac ctg tgt			939
Asp Ile Leu Leu Asp Trp Ser Met His Asn Ile Leu Trp Tyr Leu Cys			
255	260	265	
gga att tca gct ttc ctc atg caa aag gat ttt gta tcc ccg gcc tac			987
Gly Ile Ser Ala Phe Leu Met Gln Lys Asp Phe Val Ser Pro Ala Tyr			
270	275	280	285
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Leu Lys Lys Trp Ser Ala Lys Gly Ile Gln Val Val Gly Trp Thr Val			

290	295	300	
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Asn Thr Phe Asp Glu Lys Ser Tyr Tyr Glu Ser His Leu Gly Ser Ser			
305	310	315	
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Tyr Ile Thr Asp Ser Met Val Glu Asp Cys Glu Pro His Phe			
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<211> 331

<212> PRT

<213> Homo sapiens

<400> 154

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Leu Leu Thr Gly Ser Leu Phe Val Leu Leu Arg Val Phe Ser Phe Glu

35 40 45

Pro Val Pro Ser Cys Arg Ala Leu Gln Val Leu Lys Pro Arg Asp Arg

50 55 60

Ile Ser Ala Ile Ala His Arg Gly Gly Ser His Asp Ala Pro Glu Asn

65 70 75 80

Thr Leu Ala Ala Ile Arg Gln Ala Ala Lys Asn Gly Ala Thr Gly Val

85 90 95

Glu Leu Asp Ile Glu Phe Thr Ser Asp Gly Ile Pro Val Leu Met His

100 105 110

Asp Asn Thr Val Asp Arg Thr Thr Asp Gly Thr Gly Arg Leu Cys Asp

115 120 125

Leu Thr Phe Glu Gln Ile Arg Lys Leu Asn Pro Ala Ala Asn His Arg

130 135 140

Leu Arg Asn Asp Phe Pro Asp Glu Lys Ile Pro Thr Leu Arg Glu Ala

145 150 155 160

Val Ala Glu Cys Leu Asn His Asn Leu Thr Ile Phe Phe Asp Val Lys

165 170 175

Gly His Ala His Lys Ala Thr Glu Ala Leu Lys Lys Met Tyr Met Glu

180

185

190

Phe Pro Gln Leu Tyr Asn Asn Ser Val Val Cys Ser Phe Leu Pro Glu

195

200

205

Val Ile Tyr Lys Met Arg Gln Thr Asp Arg Asp Val Ile Thr Ala Leu

210

215

220

Thr His Arg Pro Trp Ser Leu Ser His Thr Gly Asp Gly Lys Pro Arg

225

230

235

240

Tyr Asp Thr Phe Trp Lys His Phe Ile Phe Val Met Met Asp Ile Leu

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255

Leu Asp Trp Ser Met His Asn Ile Leu Trp Tyr Leu Cys Gly Ile Ser

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265

270

Ala Phe Leu Met Gln Lys Asp Phe Val Ser Pro Ala Tyr Leu Lys Lys

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280

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Trp Ser Ala Lys Gly Ile Gln Val Val Gly Trp Thr Val Asn Thr Phe

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Asp Ser Met Val Glu Asp Cys Glu Pro His Phe

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<211> 3377

<212> DNA

<213> Homo sapiens

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<221> CDS

<222> (44).. (1666)

<400> 155

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Gln Arg Val Gly Ala Ala Ala Ser Arg Gly Ala Asp Asp Ala Met Glu
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Ser Ser Lys Pro Gly Pro Val Gln Val Val Leu Val Gln Lys Asp Gln
           25             30             35
cat tcc ttt gag cta gat gag aaa gcc ttg gcc agc atc ctc ttg cag    199
His Ser Phe Glu Leu Asp Glu Lys Ala Leu Ala Ser Ile Leu Leu Gln
           40             45             50
gac cac atc cga gat ctt gat gtg gtg gtg gtt tca gtg gct ggt gcc    247
Asp His Ile Arg Asp Leu Asp Val Val Val Val Ser Val Ala Gly Ala
           55             60             65
ttc cga aag ggc aag tcc ttc att ctg gat ttt atg cta cga tac tta    295
Phe Arg Lys Gly Lys Ser Phe Ile Leu Asp Phe Met Leu Arg Tyr Leu
           70             75             80
tat tct cag aag gaa agt ggc cat tca aat tgg ttg ggt gac cca gaa    343
Tyr Ser Gln Lys Glu Ser Gly His Ser Asn Trp Leu Gly Asp Pro Glu
           85             90             95             100
gaa ccg tta aca gga ttt tcc tgg aga ggg gga tct gat cca gaa acc    391
Glu Pro Leu Thr Gly Phe Ser Trp Arg Gly Gly Ser Asp Pro Glu Thr
           105             110             115
act ggg att caa atc tgg agt gaa gtt ttc act gtg gag aag cca ggt    439

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 Gly Lys Lys Val Ala Val Val Leu Met Asp Thr Gln Gly Ala Phe Asp
 135 140 145
 agc cag tca act gtg aaa gac tgt gct acc atc ttt gct cta agc act 535
 Ser Gln Ser Thr Val Lys Asp Cys Ala Thr Ile Phe Ala Leu Ser Thr
 150 155 160
 atg act agt tct gtt cag att tat aat tta tct cag aac att caa gaa 583
 Met Thr Ser Ser Val Gln Ile Tyr Asn Leu Ser Gln Asn Ile Gln Glu
 165 170 175 180
 gat gat ctt caa cag ctg cag ctc ttc aca gaa tac ggt cgt ctg gca 631
 Asp Asp Leu Gln Gln Leu Gln Leu Phe Thr Glu Tyr Gly Arg Leu Ala
 185 190 195
 atg gat gaa att ttc caa aag cct ttc cag aca ctg atg ttt ttg gtt 679
 Met Asp Glu Ile Phe Gln Lys Pro Phe Gln Thr Leu Met Phe Leu Val
 200 205 210
 aga gat tgg agt ttc cct tat gaa tat agc tat gga ctc caa gga gga 727
 Arg Asp Trp Ser Phe Pro Tyr Glu Tyr Ser Tyr Gly Leu Gln Gly Gly
 215 220 225
 atg gca ttt ttg gat aag cgt tta cag gtg aag gaa cat caa cat gaa 775
 Met Ala Phe Leu Asp Lys Arg Leu Gln Val Lys Glu His Gln His Glu
 230 235 240
 gaa att cag aat gtt cga aat cac att cac tca tgt ttc tcc gat gtc 823
 Glu Ile Gln Asn Val Arg Asn His Ile His Ser Cys Phe Ser Asp Val
 245 250 255 260

acc tgc ttt ctc tta cca cat cca gga ctc cag gtg gcc aca agc cct 871
Thr Cys Phe Leu Leu Pro His Pro Gly Leu Gln Val Ala Thr Ser Pro
265 270 275

gac ttt gat ggg aaa tta aaa gat att gct ggt gaa ttc aaa gag cag 919
Asp Phe Asp Gly Lys Leu Lys Asp Ile Ala Gly Glu Phe Lys Glu Gln
280 285 290

tta cag gca ctg ata ccg tat gta tta aac cca tct aag tta atg gaa 967
Leu Gln Ala Leu Ile Pro Tyr Val Leu Asn Pro Ser Lys Leu Met Glu
295 300 305

aag gag atc aat ggc tca aag gtc acc tgt cgg gga cta ctg gag tat 1015
Lys Glu Ile Asn Gly Ser Lys Val Thr Cys Arg Gly Leu Leu Glu Tyr
310 315 320

ttt aag gca tat att aaa att tat caa gga gaa gat ctg cct cac ccc 1063
Phe Lys Ala Tyr Ile Lys Ile Tyr Gln Gly Glu Asp Leu Pro His Pro
325 330 335 340

aag tcc atg ctt cag gcc act gct gaa gcc aac aac tta gca gct gca 1111
Lys Ser Met Leu Gln Ala Thr Ala Glu Ala Asn Asn Leu Ala Ala Ala
345 350 355

gcc tct gcc aag gac att tat tat aac aac atg gaa gag gtt tgt ggg 1159
Ala Ser Ala Lys Asp Ile Tyr Tyr Asn Asn Met Glu Glu Val Cys Gly
360 365 370

gga gag aaa cct tat ttg tct cca gac att cta gag gag aag cac tgt 1207
Gly Glu Lys Pro Tyr Leu Ser Pro Asp Ile Leu Glu Glu Lys His Cys
375 380 385

gaa ttc aaa caa ctt gct ctg gac cat ttt aag aag acc aag aag atg 1255
Glu Phe Lys Gln Leu Ala Leu Asp His Phe Lys Lys Thr Lys Lys Met
390 395 400

ggt ggg aag gat ttc agc ttt cgt tac cag cag gag ctg gag gag gaa 1303
 Gly Gly Lys Asp Phe Ser Phe Arg Tyr Gln Gln Glu Leu Glu Glu Glu
 405 410 415 420
 atc aag gaa tta tat gag aac ttc tgc aag cac aat ggt agc aag aac 1351
 Ile Lys Glu Leu Tyr Glu Asn Phe Cys Lys His Asn Gly Ser Lys Asn
 425 430 435
 gtc ttc agc acc ttc cga acc cct gca gtg ctg ttc acg ggc att gta 1399
 Val Phe Ser Thr Phe Arg Thr Pro Ala Val Leu Phe Thr Gly Ile Val
 440 445 450
 gct ttg tac ata gcc tca ggc ctc act ggc ttc ata ggt ctt gag gtt 1447
 Ala Leu Tyr Ile Ala Ser Gly Leu Thr Gly Phe Ile Gly Leu Glu Val
 455 460 465
 gla gcc cag ttg ttc aac tgt atg gtt gga cta ctg tta ata gca ctc 1495
 Val Ala Gln Leu Phe Asn Cys Met Val Gly Leu Leu Leu Ile Ala Leu
 470 475 480
 ctc acc tgg ggc tac atc agg tat tct ggt caa tat cgt gag ctg ggc 1543
 Leu Thr Trp Gly Tyr Ile Arg Tyr Ser Gly Gln Tyr Arg Glu Leu Gly
 485 490 495 500
 gga gct att gat ttt ggt gcc gca tat gtg ttg gag cag gct tct tct 1591
 Gly Ala Ile Asp Phe Gly Ala Ala Tyr Val Leu Glu Gln Ala Ser Ser
 505 510 515
 cat atc ggt aat tcc act cag gcc act gtg agg gat gca gtt gtt gga 1639
 His Ile Gly Asn Ser Thr Gln Ala Thr Val Arg Asp Ala Val Val Gly
 520 525 530
 aga cca tcc atg gat aaa aaa gct caa tagcatctta acgtgaagat 1686
 Arg Pro Ser Met Asp Lys Lys Ala Gln

535

540

caaacaagaa cacaacaagc ccctactgat ttctlggttt ctgccacggc cacaggttca 1746
tatccagagg aatggcagat ctgagacgat ccaggaagag ctaaaacalg gccctgtaat 1806
aaatgagcag acctctcctg tggtttcaaa ttattaaaca cacttccatt tctcttggaa 1866
gcatttcttt tcttctctgt tatagaigca agcctgtgtc tattttcata ttactctgct 1926
ttgtgcactt tatggaggag gaagctagag gaaaaatgga aatgcagctt ttaagtctt 1986
tatgtgccac ttagtgccct ttaagattga ttccatggtt ttgcacacac gatggggagg 2046
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actttacttt tgagaaggat tctttttttt ttgagttgga gtctcgtct gtaccaggc 2166
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ttcagaacta aagactaact gaaaatgat tcattacact caaaaaaaaa ttacaatagg 2526
gaatccgtt gccacatagt gtggaaaaat catgtcata ttaaataac catactctga 2586
aatgtagggt ttttaccag taggtgaca gttttgtgc aacttgcct atttttttt 2646
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taacigtgtt ggggggtggg ggagatgaaa gagagtcgct tttgtttac agttaaagac 3126
atccaatac ttaaaaagga gtttcttct agaaacacac acaccttcc tctgtctcaa 3186
aagatctcac tccatgatac tgtgtaaaat attttgcac tgttgtgaag tatttttgac 3246

ttttttctgt acataactgt gtctcagag ctgaatgttt atatcttttg ctgtgcaaaa 3306
 gaaacatgta aaatgttgtt cagttgtata tacagaaaag tgtataaaac atttgttat 3366
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<210> 156

<211> 541

<212> PRT

<213> Homo sapiens

<400> 156

Met Leu Ser Pro Gln Arg Val Gly Ala Ala Ala Ser Arg Gly Ala Asp
 1 5 10 15
 Asp Ala Met Glu Ser Ser Lys Pro Gly Pro Val Gln Val Val Leu Val
 20 25 30
 Gln Lys Asp Gln His Ser Phe Glu Leu Asp Glu Lys Ala Leu Ala Ser
 35 40 45
 Ile Leu Leu Gln Asp His Ile Arg Asp Leu Asp Val Val Val Val Ser
 50 55 60
 Val Ala Gly Ala Phe Arg Lys Gly Lys Ser Phe Ile Leu Asp Phe Met
 65 70 75 80
 Leu Arg Tyr Leu Tyr Ser Gln Lys Glu Ser Gly His Ser Asn Trp Leu
 85 90 95
 Gly Asp Pro Glu Glu Pro Leu Thr Gly Phe Ser Trp Arg Gly Gly Ser
 100 105 110
 Asp Pro Glu Thr Thr Gly Ile Gln Ile Trp Ser Glu Val Phe Thr Val
 115 120 125
 Glu Lys Pro Gly Gly Lys Lys Val Ala Val Val Leu Met Asp Thr Gln
 130 135 140

Gly Ala Phe Asp Ser Gln Ser Thr Val Lys Asp Cys Ala Thr Ile Phe
 145 150 155 160
 Ala Leu Ser Thr Met Thr Ser Ser Val Gln Ile Tyr Asn Leu Ser Gln
 165 170 175
 Asn Ile Gln Glu Asp Asp Leu Gln Gln Leu Gln Leu Phe Thr Glu Tyr
 180 185 190
 Gly Arg Leu Ala Met Asp Glu Ile Phe Gln Lys Pro Phe Gln Thr Leu
 195 200 205
 Met Phe Leu Val Arg Asp Trp Ser Phe Pro Tyr Glu Tyr Ser Tyr Gly
 210 215 220
 Leu Gln Gly Gly Met Ala Phe Leu Asp Lys Arg Leu Gln Val Lys Glu
 225 230 235 240
 His Gln His Glu Glu Ile Gln Asn Val Arg Asn His Ile His Ser Cys
 245 250 255
 Phe Ser Asp Val Thr Cys Phe Leu Leu Pro His Pro Gly Leu Gln Val
 260 265 270
 Ala Thr Ser Pro Asp Phe Asp Gly Lys Leu Lys Asp Ile Ala Gly Glu
 275 280 285
 Phe Lys Glu Gln Leu Gln Ala Leu Ile Pro Tyr Val Leu Asn Pro Ser
 290 295 300
 Lys Leu Met Glu Lys Glu Ile Asn Gly Ser Lys Val Thr Cys Arg Gly
 305 310 315 320
 Leu Leu Glu Tyr Phe Lys Ala Tyr Ile Lys Ile Tyr Gln Gly Glu Asp
 325 330 335
 Leu Pro His Pro Lys Ser Met Leu Gln Ala Thr Ala Glu Ala Asn Asn
 340 345 350

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Leu Ala Ala Ala Ala Ser Ala Lys Asp Ile Tyr Tyr Asn Asn Met Glu
 355 360 365
 Glu Val Cys Gly Gly Glu Lys Pro Tyr Leu Ser Pro Asp Ile Leu Glu
 370 375 380
 Glu Lys His Cys Glu Phe Lys Gln Leu Ala Leu Asp His Phe Lys Lys
 385 390 395 400
 Thr Lys Lys Met Gly Gly Lys Asp Phe Ser Phe Arg Tyr Gln Gln Glu
 405 410 415
 Leu Glu Glu Glu Ile Lys Glu Leu Tyr Glu Asn Phe Cys Lys His Asn
 420 425 430
 Gly Ser Lys Asn Val Phe Ser Thr Phe Arg Thr Pro Ala Val Leu Phe
 435 440 445
 Thr Gly Ile Val Ala Leu Tyr Ile Ala Ser Gly Leu Thr Gly Phe Ile
 450 455 460
 Gly Leu Glu Val Val Ala Gln Leu Phe Asn Cys Met Val Gly Leu Leu
 465 470 475 480
 Leu Ile Ala Leu Leu Thr Trp Gly Tyr Ile Arg Tyr Ser Gly Gln Tyr
 485 490 495
 Arg Glu Leu Gly Gly Ala Ile Asp Phe Gly Ala Ala Tyr Val Leu Glu
 500 505 510
 Gln Ala Ser Ser His Ile Gly Asn Ser Thr Gln Ala Thr Val Arg Asp
 515 520 525
 Ala Val Val Gly Arg Pro Ser Met Asp Lys Lys Ala Gln
 530 535 540

<210> 157

<211> 2172

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (45).. (563)

<400> 157

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Met Asp Asp Ala

1

ccg ggc gac ccg cgg caa ccc cac cgc ccc gac ccc ggc cgc cca gtg 104

Pro Gly Asp Pro Arg Gln Pro His Arg Pro Asp Pro Gly Arg Pro Val

5

10

15

20

ggc ctg gag cag ctg cgg cgg ctc ggg gtg ctc tac tgg aag ctg gat 152

Gly Leu Glu Gln Leu Arg Arg Leu Gly Val Leu Tyr Trp Lys Leu Asp

25

30

35

gct gac aaa tat gag aat gat cca gaa tta gaa aag atc cga aga gag 200

Ala Asp Lys Tyr Glu Asn Asp Pro Glu Leu Glu Lys Ile Arg Arg Glu

40

45

50

agg aac tac tcc tgg atg gac atc ata acc ata tgc aaa gat aaa cta 248

Arg Asn Tyr Ser Trp Met Asp Ile Ile Thr Ile Cys Lys Asp Lys Leu

55

60

65

cca aat tat gaa gaa aag att aag atg ttc tac gag gag cat ttg cac 296

Pro Asn Tyr Glu Glu Lys Ile Lys Met Phe Tyr Glu Glu His Leu His

70

75

80

ttg gac gat gag atc cgc tac atc ctg gat ggc agt ggg tac ttc gat 344

Leu Asp Asp Glu Ile Arg Tyr Ile Leu Asp Gly Ser Gly Tyr Phe Asp

85

90

95

100

gig agg gac aag gag gac cag tgg atc cgg atc ttc atg gag aag gga 392

Val Arg Asp Lys Glu Asp Gln Trp Ile Arg Ile Phe Met Glu Lys Gly

105

110

115

gac atg gig acg ctc ccc gcg ggg atc tat cac cgc ttc acg gtg gac 440

Asp Met Val Thr Leu Pro Ala Gly Ile Tyr His Arg Phe Thr Val Asp

120

125

130

gag aag aac tac acg aag gcc atg cgg ctg ttt gig gga gaa ccg gig 488

Glu Lys Asn Tyr Thr Lys Ala Met Arg Leu Phe Val Gly Glu Pro Val

135

140

145

tgg aca gcg tac aac cgg ccc gct gac cat ttt gaa gcc cgc ggg cag 536

Trp Thr Ala Tyr Asn Arg Pro Ala Asp His Phe Glu Ala Arg Gly Gln

150

155

160

tac gtg aaa ttt ctg gca cag acc gcc tagcagtgtt gccctgggaac 583

Tyr Val Lys Phe Leu Ala Gln Thr Ala

165

170

taacacgtgc ctctgtaaagg tccccaatgt aatgactgag cagaaaaatca atcacatttct 643

ctttgtcttt agaggatagc cttagaggcta gattatcttt cctttglaag attatttgat 703

cagaatattt tgaatgaaa ggaatctagaa agcaacttgg aagtglaaag agtcaccttc 763

atittctgta actcaatcaa gactgggtggg tccatggccc tgtgttagtt catgattca 823

gttaggtccc aatgaaagt ttcatctccc gaaatgcagt tccttagatg cccatctgga 883

cgtgatgccg cgccgccgt gtaagaaggt gcaatcctag ataacacagc tagccagata 943

gaagacactt tttctccaa aatgatgcct tgggggtggg agtggtaggg ggaagagctc 1003

ccaccctaag gggcacacac tgagttgctt atgccacttc ctgttcaaa ataaagtaac 1063

tgccttaac ttataactcat ggcttggagt taccttatat tcaggtatat gtgatatttt 1123

gccigtgttg ttaaaattgc cccatttaga ttctttctat aattgttctt atagataagt 1183

aatitatata tgagctgtgt tagtattttt tcagtgtgag atctctggat tctttcacia 1243

taaagctggt gaattttaac aggagiatta gtacataaat ttcttactca acaattccga 1303
 gataggatta tgcctagttt gtcataacac agaaaaactc caagttaact tcatgttttg 1363
 gaagggcagg tcgtttttta agtatttctt tttttaactg gatgaaaaat ctcatgttta 1423
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 agtaaactct gtctcagttt taggattaaa ataccacccg gtggigtgat gatgccatat 1543
 accgcagggc ttgcttctgt caagtgtgac tctatctcag taattaaaaat aagtgcgtgat 1603
 ctactgattt tttttaatgg atcatttctt aaatgggcat tataaataga gcttgttcat 1663
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 caggaggcta aggtgggagg attcttagag ccgtggaggt cgaggctgca gtgagctgtg 1963
 attgtggcca ctgcacacca gccgtgggtg cagagcgaga ctctgtctca aaaaagaaga 2023
 aagagtaaga gctgaggcat ataataaat tctgtctaaag cacttaaggt gaaatcacat 2083
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 ataaaatgta ctcattttca gtgtttttg 2172

<210> 158

<211> 173

<212> PRT

<213> Homo sapiens

<400> 158

Met Asp Asp Ala Pro Gly Asp Pro Arg Gln Pro His Arg Pro Asp Pro

1 5 10 15

Gly Arg Pro Val Gly Leu Glu Gln Leu Arg Arg Leu Gly Val Leu Tyr

20 25 30

Trp Lys Leu Asp Ala Asp Lys Tyr Glu Asn Asp Pro Glu Leu Glu Lys

35 40 45
Ile Arg Arg Glu Arg Asn Tyr Ser Trp Met Asp Ile Ile Thr Ile Cys
50 55 60
Lys Asp Lys Leu Pro Asn Tyr Glu Glu Lys Ile Lys Met Phe Tyr Glu
65 70 75 80
Glu His Leu His Leu Asp Asp Glu Ile Arg Tyr Ile Leu Asp Gly Ser
85 90 95
Gly Tyr Phe Asp Val Arg Asp Lys Glu Asp Gln Trp Ile Arg Ile Phe
100 105 110
Met Glu Lys Gly Asp Met Val Thr Leu Pro Ala Gly Ile Tyr His Arg
115 120 125
Phe Thr Val Asp Glu Lys Asn Tyr Thr Lys Ala Met Arg Leu Phe Val
130 135 140
Gly Glu Pro Val Trp Thr Ala Tyr Asn Arg Pro Ala Asp His Phe Glu
145 150 155 160
Ala Arg Gly Gln Tyr Val Lys Phe Leu Ala Gln Thr Ala
165 170

<210> 159

<211> 20

<212> DNA

<220>

<223> Description of the artificial sequence: an artificially synthesized primer sequence

<400> 159

ggaagtgtta ctctgctct

20

<210> 160

<211> 50

<212> DNA

<220>

<223> Description of the artificial sequence: an artificially synthesized primer sequence

<400> 160

gagagagaga gagagagaga actagtcicg agtttttttt tttttttttt 50

<210> 161

<211> 41

<212> DNA

<220>

<223> Description of the artificial sequence: an artificially synthesized primer sequence

<400> 161

gagagagaga gagagagcgg ccgcactagt ccccccccc c 41

<210> 162

<211> 30

<212> RNA

<213> Artificial Sequence

<220>

<223> Description of the artificial sequence: an artificially synthesized oligo-cap linker sequence

<400> 162

agcaucgagu cggccuuguu ggccuacugg 30

<210> 163

<211> 42

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of the artificial sequence: an artificially synthesized oligo(dT) primer sequence

<400> 163

gcggctgaag acggcctatg tggccttttt tttttttttt tt 42

<210> 164
 <211> 21
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Description of the artificial sequence: an artificially synthesized primer
 sequence
 <400> 164
 agcatcgagt cggccttggt g 21

<210> 165
 <211> 21
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Description of the artificial sequence: an artificially synthesized primer
 sequence
 <400> 165
 gcggctgaag acggcctatg t 21

<210> 166
 <211> 30
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Description of the artificial sequence: an artificially synthesized primer
 sequence
 <400> 166
 actttattgt catagtttag atctatttg 30

<210> 167
 <211> 30
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Description of the artificial sequence: an artificially synthesized primer
 sequence
 <400> 167
 ataatccita aaaactccat ttccaccct 30

<210> 168
 <211> 1536
 <212> DNA
 <213> Homo sapiens
 <220>
 <221> CDS
 <222> (139).. (1062)
 <400> 168
 GTGCTCCGCC GCCCGCCCCG ACCCGGGCCC AGCCGCCTCC ACGGCCCCGCG CTCGTA CTGG 60
 AGCGAAGAGC GGCCTCCTGA GGGAGGGGAA GGGACGTGGG GGCGGCCACG GCAGGATTAA 120
 CCTCCATTTC AGCTAATC ATG GGA GAG ATT AAA GTC TCT CCT GAT TAT AAC 171
 Met Gly Glu Ile Lys Val Ser Pro Asp Tyr Asn
 1 5 10

TGG TTT AGA GGT ACA GTT CCC CTT AAA AAG ATT ATT GTG GAT GAT GAT Trp Phe Arg Gly Thr Val Pro Leu Lys Lys Ile Ile Val Asp Asp Asp 15 20 25	219
GAC AGT AAG ATA TGG TCG CTC TAT GAC GCG GGC CCC CGA AGT ATC AGG Asp Ser Lys Ile Trp Ser Leu Tyr Asp Ala Gly Pro Arg Ser Ile Arg 30 35 40	267
TGT CCT CTC ATA TTC CTG CCC CCT GTC AGT GGA ACT GCA GAT GTC TTT Cys Pro Leu Ile Phe Leu Pro Pro Val Ser Gly Thr Ala Asp Val Phe 45 50 55	315
TTC CGG CAG ATT TTG GCT CTG ACT GGA TGG GGT TAC CGG GTT ATC GCT Phe Arg Gln Ile Leu Ala Leu Thr Gly Trp Gly Tyr Arg Val Ile Ala 60 65 70 75	363
TTG CAG TAT CCA GTT TAT TGG GAC CAT CTC GAG TTC TGT GAT GGA TTC Leu Gln Tyr Pro Val Tyr Trp Asp His Leu Glu Phe Cys Asp Gly Phe 80 85 90	411
AGA AAA CTT TTA GAC CAT TTA CAA TTG GAT AAA GTT CAT CTT TTT GGC Arg Lys Leu Leu Asp His Leu Gln Leu Asp Lys Val His Leu Phe Gly 95 100 105	459
GCT TCT TTG GGA GGC TTT TTG GCC CAG AAA TTT GCT GAA TAT ACT CAC Ala Ser Leu Gly Gly Phe Leu Ala Gln Lys Phe Ala Glu Tyr Thr His 110 115 120	507
AAA TCT CCT AGA GTC CAT TCC CTA ATC CTC TGC AAT TCC TTC AGT GAC Lys Ser Pro Arg Val His Ser Leu Ile Leu Cys Asn Ser Phe Ser Asp 125 130 135	555
ACC TCT ATC TTC AAC CAA ACT TGG ACT GCA AAC AGC TTT TGG CTG ATG Thr Ser Ile Phe Asn Gln Thr Trp Thr Ala Asn Ser Phe Trp Leu Met 140 145 150 155	603
CCT GCA TTT ATG CTC AAA AAA ATA GTT CTT GGA AAT TTT TCA TCT GGC Pro Ala Phe Met Leu Lys Lys Ile Val Leu Gly Asn Phe Ser Ser Gly 160 165 170	651
CCG GTG GAC CCT ATG ATG GCT GAT GCC ATT GAT TTC ATG GTA GAC AGG Pro Val Asp Pro Met Met Ala Asp Ala Ile Asp Phe Met Val Asp Arg 175 180 185	699
CTA GAA AGT TTG GGT CAG AGT GAA CTG GCT TCA AGA CTT ACC TTG AAT Leu Glu Ser Leu Gly Gln Ser Glu Leu Ala Ser Arg Leu Thr Leu Asn 190 195 200	747
TGT CAA AAT TCT TAT GTG GTA CCT CAT AAA ATT CGG GAC ATA CCT GTA Cys Gln Asn Ser Tyr Val Val Pro His Lys Ile Arg Asp Ile Pro Val 205 210 215	795

ACT ATT ATG GAT GTG TTT GAT CAG AGT GCG CTT TCA ACT GAA GCT AAA Thr Ile Met Asp Val Phe Asp Gln Ser Ala Leu Ser Thr Glu Ala Lys 220 225 230 235	843
GAA GAA ATG TAC AAG CTG TAT CCT AAT GCC CGA AGA GCT CAT CTG AAA Glu Glu Met Tyr Lys Leu Tyr Pro Asn Ala Arg Arg Ala His Leu Lys 240 245 250	891
ACA GGA GGC AAT TTC CCA TAC CTG TGC AGA AGT GCA GAG GTC AAT CTT Thr Gly Gly Asn Phe Pro Tyr Leu Cys Arg Ser Ala Glu Val Asn Leu 255 260 265	939
TAT GTA CAG ATA CAT TTG CTG CAA TTC CAT GGA ACC AAA TAC GCG GCC Tyr Val Gln Ile His Leu Leu Gln Phe His Gly Thr Lys Tyr Ala Ala 270 275 280	987
ATT GAC CCA TCA ATG GTC AGT GCC GAG GAG CTT GAG GTG CAG AAA GGC Ile Asp Pro Ser Met Val Ser Ala Glu Glu Leu Glu Val Gln Lys Gly 285 290 295	1035
AGC CTT GGC ATC AGC CAG GAG GAG CAG TAGTGTGTCT CTCGCTGTCA ATGATGA Ser Leu Gly Ile Ser Gln Glu Glu Gln 300 305	1089
GTTGACCCGG TGTGTTCTTG TATAGTCAGT GGCATCAGCA CCCGTCAGCC GGCCTTTTCC TTCAGGTTTCG TCAGGCTCAC CGGTTCTCAC TGTGTCTGGG AAGTAGGACT GATGGTCATC TTCATGACAG GCGGCATCTC CACTAAGCCT GTGTAACGT TCCCTCTTTG GTTTTCTTAG CTTTTGAATT TGAAGAAGTA CTTTGAAGA CTCCCATTTT AAGAACCGTG CAGATTTTGC TACCAAAAGT CTTCAACCACT GTGTTCTTAA GTGAATGTTA ATTTCTGAGG TTTGGGACTT TGTGGTGTT TTTTCTTCT TTTCTTTTCC ATTCTTCTTT CTTCTTTTT ATGTTGTTTG CTGTAAATGC TGCACATCCA GATTGCATAT CAGGACATTG GTTATTTTAT GCTTTCTTGG ATATAACCAT GATCAGAGTG CCATGGC	1149 1209 1269 1329 1389 1449 1509 1536
<210> 169	
<211> 308	
<212> PRT	
<213> Homo sapiens	
<400> 169	
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115 120 125
 His Ser Leu Ile Leu Cys Asn Ser Phe Ser Asp Thr Ser Ile Phe Asn
 130 135 140
 Gln Thr Trp Thr Ala Asn Ser Phe Trp Leu Met Pro Ala Phe Met Leu
 145 150 155 160
 Lys Lys Ile Val Leu Gly Asn Phe Ser Ser Gly Pro Val Asp Pro Met
 165 170 175
 Met Ala Asp Ala Ile Asp Phe Met Val Asp Arg Leu Glu Ser Leu Gly
 180 185 190
 Gln Ser Glu Leu Ala Ser Arg Leu Thr Leu Asn Cys Gln Asn Ser Tyr
 195 200 205
 Val Val Pro His Lys Ile Arg Asp Ile Pro Val Thr Ile Met Asp Val
 210 215 220
 Phe Asp Gln Ser Ala Leu Ser Thr Glu Ala Lys Glu Glu Met Tyr Lys
 225 230 235 240
 Leu Tyr Pro Asn Ala Arg Arg Ala His Leu Lys Thr Gly Gly Asn Phe
 245 250 255
 Pro Tyr Leu Cys Arg Ser Ala Glu Val Asn Leu Tyr Val Gln Ile His
 260 265 270
 Leu Leu Gln Phe His Gly Thr Lys Tyr Ala Ala Ile Asp Pro Ser Met
 275 280 285
 Val Ser Ala Glu Glu Leu Glu Val Gln Lys Gly Ser Leu Gly Ile Ser
 290 295 300
 Gln Glu Glu Gln
 305

<210> 170

<211> 2560

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

(202).. (1002)

<400> 170

CTGGCCTACT GGGGCTCCAG CCGTGTCTTG AGGAGCTGGA CCAGCCACAT CCCCTGGGGC 60
 TGCAGTTGAA GCAGAACCAA GTGGCCATCC CGGCGTTAGA CCGTAGGTTC CTGGTCCCGG 120
 AGTGGTCGGA GCGGCCAGT GGGCAGGCAG CTCTTGCTCA CAGGCCGCGG TGCCAGGCC 180
 GCTGGCTCTC CGCAGGGCGG A ATG GCG CTG CAA GTG GAG CTG GTA CCC ACC 231
 Met Ala Leu Gln Val Glu Leu Val Pro Thr
 1 5 10

GGG GAG ATC ATC CGC GTG GTT CAT CCC CAC AGG CCC TGC AAG CTT GCC 279
 Gly Glu Ile Ile Arg Val Val His Pro His Arg Pro Cys Lys Leu Ala
 15 20 25

CTG GGC AGT GAC GGG GTT CGG GTG ACC ATG GAG AGT GCG CTC ACC GCC 327
 Leu Gly Ser Asp Gly Val Arg Val Thr Met Glu Ser Ala Leu Thr Ala
 30 35 40

CGT GAC CGG GTG GGG GTG CAG GAT TTC GTG CTG CTG GAG AAC TTC ACC 375
 Arg Asp Arg Val Gly Val Gln Asp Phe Val Leu Leu Glu Asn Phe Thr
 45 50 55

AGC GAG GCC GCC TTC ATC GGG AAC CTG CGG CGG CGA TTT CGG GAG AAT Ser Glu Ala Ala Phe Ile Gly Asn Leu Arg Arg Arg Phe Arg Glu Asn 60 65 70	423
CTC ATC TAC ACC TAC ATT GGC CCC GTC CTG GTC TCT GTC AAT CCC TAC Leu Ile Tyr Thr Tyr Ile Gly Pro Val Leu Val Ser Val Asn Pro Tyr 75 80 85 90	471
CGG GAC CTG CAG ATC TAC AGC CGG CAG CAT ATG GAG CGT TAC CGT GGC Arg Asp Leu Gln Ile Tyr Ser Arg Gln His Met Glu Arg Tyr Arg Gly 95 100 105	519
GTC AGC TTC TAT GAA GTG CCC CCT CAC CTG TTT GCC GTG GCG GAC ACT Val Ser Phe Tyr Glu Val Pro Pro His Leu Phe Ala Val Ala Asp Thr 110 115 120	567
GTG TAC CGA GCA CTG CGC ACG GAG CGT CGG GAC CAG GCT GTG ATG ATC Val Tyr Arg Ala Leu Arg Thr Glu Arg Arg Asp Gln Ala Val Met Ile 125 130 135	615
TCT GGG GAG AGC GGG GCA GGC AAG ACC GAG GCC ACC AAG AGG CTG CTG Ser Gly Glu Ser Gly Ala Gly Lys Thr Glu Ala Thr Lys Arg Leu Leu 140 145 150	663
CAG TTC TAT GCA GAG ACC TGC CCA GCC CCC GAG CGC GGA GGT GCC GTG Gln Phe Tyr Ala Glu Thr Cys Pro Ala Pro Glu Arg Gly Gly Ala Val 155 160 165 170	711
CGG GAC CGG CTG CTA CAG AGC AAC CCG GTG CTG GAG GCC TTT GGA AAT Arg Asp Arg Leu Leu Gln Ser Asn Pro Val Leu Glu Ala Phe Gly Asn 175 180 185	759
GCC AAG ACC CTC CGG AAC GAT AAC TCC AGC AGG TTC GGG AAG TAC ATG Ala Lys Thr Leu Arg Asn Asp Asn Ser Ser Arg Phe Gly Lys Tyr Met 190 195 200	807
GAT GTG CAG TTT GAC TTC AAG GGT GCC CCC GTG GGT GGC CAC ATC CTC Asp Val Gln Phe Asp Phe Lys Gly Ala Pro Val Gly Gly His Ile Leu 205 210 215	855
AGT TAC CCC CTG GAA AAG TCA CGA GTG GTG CAC CAG AAT CAT GGG GAG Ser Tyr Pro Leu Glu Lys Ser Arg Val Val His Gln Asn His Gly Glu 220 225 230	903
CGG AAC TTC ACA TCT TCT ACC AGC TGC TGG AGG GGG GCG AGG AGG AGA Arg Asn Phe Thr Ser Ser Thr Ser Cys Trp Arg Gly Ala Arg Arg Arg 235 240 245 250	951
CTC TTC GCA GGC TGG GCT TGG AAC GGA ACC CCC AGA GCT ATC TGT ACC Leu Phe Ala Gly Trp Ala Trp Asn Gly Thr Pro Arg Ala Ile Cys Thr 255 260 265	999
TGG TGAAGGCCAG TGTGCCAAAG TCTTCTTCAT CAACGACAAG AGTGACTGGA AGGTGCG	1058

Trp

TCAGGAAGGC TCTGACAGTC ATTGATTTC CCGAGGATGA AGTGGAGGAC CTGCTGAGCA 1118
 TCGTGGCCAG CGTCCTTCAT TTGGGCAACA TCCACTTTGC TGCCAACGAG GAGAGCAATG 1178
 CCCAGGTCAC CACCGAGAAC CAGCTCAAGT ATCTGAGCCC ATTCAGTATG CCGTGCCTGT 1238
 TGTGAAATAC GACCGCAAGG GCTACAAGCC TCGCTCCCGG CAGCTGCTGC TCACGCCCAA 1298
 CGCCGTCGTC ATCGTGAGG ACGCCAAAGT CAAGCAGAGG ATTGATTACG CCAACCTGAC 1358
 CGGAATCTCT GTCAGCAGCC TGAGCGACAG TCTTTTTGTG CTTTCATGTAC AGCGTGCGGA 1418
 CAATAAGCAA AAGGGAGATG TGGTGCTGCA GAGTGACCAC GTGATTGAGA CGCTGACCAA 1478
 GACAGCCCTC AGTGCCAACC GCGTGAACAG CATCAACATC AACCAGGGCA GCATCACGTT 1538
 TGCAGGGGGC CCCGGCAGGG ATGGCACCAT TGACTTCACA CCCGGCTCGG AGCTGCTCAT 1598
 CACCAAGGCC AAGAACGGGC ACCTGGCTGT GGTGCCCCA CGGCTGAATT CTCGGTGATA 1658
 AAGGCGCCCA CTGGACCCTC CCAACGCCCA ATGCTTTGCT TTTCTCCTCC TCCCCTTCCC 1718
 AGTTACCAAA GACTCGAACT TCCAGACAGG GACCCAGGGA CACCCCGAAG CCCACCTGCA 1778
 ATCTCCCAAC TCCTGCCCAT CCCTCTCTTG AGGGAGCAGC AGGGGCCAGG AGCTACCCCA 1838
 GGAGTGGGCC AGGCCGGGCC ACAGCAATAG GAAAGCCAGG GCCAGAGCGA GCCATGCCAG 1898
 CCCTACTGCC GATGCCAAAT ATTTGAGAGA AGGGAAC TTT TGCTGAGGTT TTCTCTGAGG 1958
 TTTTTTTTGA TGCTTTATAG GAAACTATTT TTTAAAAAAA GCCATTTCCTC ACCCAAGGAC 2018
 ACAGTGGATG TGTTTTCCCT GACTCCAGCA GGGCAAGGAA ATGTAGCCGA GAGGTTGTGT 2078
 GGGCTGGGCT CTGGTGCCCT CTTCCCTGGC CAGGACACCT CTCCTCCTGA TTCCCTTGGC 2138
 ACCTTGCTTT TCTGTCTGTT TACCTGTCTC CCTGCCTGCC CATCTGCATC TTTTGCAGCC 2198
 CACTCTGACT TCCATCTGGG GGCTGAGACC ACCCTTGCTT GCCCCCTTCT TTCTGCCTTA 2258
 AGAATGTCCT TTTAGGCTGG GCATGGTGGC TCACGCCTGT AACCCAGCA CTTTGGGAGG 2318
 CGGAGACGGG CAGATAACCT GAGGTCAGGA TTTTCGAGACC AACCTGACCT ACATGGAGAA 2378
 ACTCCGCCTC TGGAAGGAT ACAAATTAG CCGGGCATGG TGGTGCACGC CTCTAATCCC 2438
 AGCTGCTCGG GAGGCTGAGG CAGGAGAATC ACTTGAACCC GGGAAGTGA GGTGACGTG 2498
 AGCCAAGAGT ACACCACTGC ACTCCAGCCT GGGCAACAGA GCGAGACTCC GTCTTAAAAA 2558
 AA 2560

<210> 171

<211> 267

<212> PRT

<213> Homo sapiens

<400> 171

Met Ala Leu Gln Val Glu Leu Val Pro Thr Gly Glu Ile Ile Arg Val
 1 5 10 15
 Val His Pro His Arg Pro Cys Lys Leu Ala Leu Gly Ser Asp Gly Val
 20 25 30
 Arg Val Thr Met Glu Ser Ala Leu Thr Ala Arg Asp Arg Val Gly Val
 35 40 45
 Gln Asp Phe Val Leu Leu Glu Asn Phe Thr Ser Glu Ala Ala Phe Ile
 50 55 60
 Gly Asn Leu Arg Arg Arg Phe Arg Glu Asn Leu Ile Tyr Thr Tyr Ile
 65 70 75 80
 Gly Pro Val Leu Val Ser Val Asn Pro Tyr Arg Asp Leu Gln Ile Tyr
 85 90 95
 Ser Arg Gln His Met Glu Arg Tyr Arg Gly Val Ser Phe Tyr Glu Val
 100 105 110
 Pro Pro His Leu Phe Ala Val Ala Asp Thr Val Tyr Arg Ala Leu Arg
 115 120 125
 Thr Glu Arg Arg Asp Gln Ala Val Met Ile Ser Gly Glu Ser Gly Ala
 130 135 140
 Gly Lys Thr Glu Ala Thr Lys Arg Leu Leu Gln Phe Tyr Ala Glu Thr

145		150		155		160									
Cys	Pro	Ala	Pro	Glu	Arg	Gly	Gly	Ala	Val	Arg	Asp	Arg	Leu	Leu	Gln
		165		170		175									
Ser	Asn	Pro	Val	Leu	Glu	Ala	Phe	Gly	Asn	Ala	Lys	Thr	Leu	Arg	Asn
		180		185		190									
Asp	Asn	Ser	Ser	Arg	Phe	Gly	Lys	Tyr	Met	Asp	Val	Gln	Phe	Asp	Phe
		195		200		205									
Lys	Gly	Ala	Pro	Val	Gly	Gly	His	Ile	Leu	Ser	Tyr	Pro	Leu	Glu	Lys
	210			215		220									
Ser	Arg	Val	Val	His	Gln	Asn	His	Gly	Glu	Arg	Asn	Phe	Thr	Ser	Ser
225				230		235									240
Thr	Ser	Cys	Trp	Arg	Gly	Ala	Arg	Arg	Arg	Leu	Phe	Ala	Gly	Trp	Ala
				245		250									255
Trp	Asn	Gly	Thr	Pro	Arg	Ala	Ile	Cys	Thr	Trp					
			260			265									

<210> 172

<211> 2650

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (116).. (1216)

<400> 172

CTTTTGCTGC	TGCGCCCGGG	CAGGGGCTGC	CGCGGCCCCA	GGTCCCGCTT	CGAGACGCGG	60
CGCGGTCCAG	GCGGGAGGCG	ACTCCCTAGG	AAGGGACCCG	GGGCGGGAGG	AGGAA ATG	118
				Met		
				1		

AGG	CCG	CGC	GGA	AGG	AAG	GCG	GCG	AGC	CCC	GGG	GCC	CCG	AGG	CCT	TGG	166
Arg	Pro	Arg	Gly	Arg	Lys	Ala	Ala	Ser	Pro	Gly	Ala	Pro	Arg	Pro	Trp	
			5					10					15			

CCG	CGT	CAC	AGC	ACC	CAC	ATG	GCC	TCT	GGA	GTG	GGC	GCG	GCC	TTC	GAG	214
Pro	Arg	His	Ser	Thr	His	Met	Ala	Ser	Gly	Val	Gly	Ala	Ala	Phe	Glu	
			20				25					30				

GAA	CTG	CCT	CAC	GAC	GGC	ACG	TGT	GAC	GAG	TGC	GAG	CCC	GAC	GAG	GCT	262
Glu	Leu	Pro	His	Asp	Gly	Thr	Cys	Asp	Glu	Cys	Glu	Pro	Asp	Glu	Ala	
	35					40					45					

CCG	GGG	GCC	GAG	GAA	GTG	TGC	CGA	GAA	TGC	GGC	TTC	TGC	TAC	TGC	CGC	310
Pro	Gly	Ala	Glu	Glu	Val	Cys	Arg	Glu	Cys	Gly	Phe	Cys	Tyr	Cys	Arg	
	50				55					60					65	

CGC	CAT	GCC	GAG	GCG	CAC	AGG	CAG	AAG	TTC	CTC	AGT	CAC	CAT	CTG	GCC	358
Arg	His	Ala	Glu	Ala	His	Arg	Gln	Lys	Phe	Leu	Ser	His	His	Leu	Ala	
				70				75						80		

GAA	TAC	GTC	CAC	GGC	TCC	CAG	GCC	TGG	ACC	CCG	CCA	GCT	GAC	GGA	GAG	406
Glu	Tyr	Val	His	Gly	Ser	Gln	Ala	Trp	Thr	Pro	Pro	Ala	Asp	Gly	Glu	
			85				90						95			

GGG GCG GGG AAG GAA GAA GCG GAG GTC AAG GTG GAG CAG GAG AGG GAG Gly Ala Gly Lys Glu Glu Ala Glu Val Lys Val Glu Gln Glu Arg Glu 100 105 110	454
ATA GAA AGC GAG GCA GGG GAA GAG AGT GAG TCG GAG GAA GAG AGC GAG Ile Glu Ser Glu Ala Gly Glu Glu Ser Glu Ser Glu Glu Glu Ser Glu 115 120 125	502
TCA GAG GAA GAG AGC GAG ACA GAG GAA GAG AGT GAG GAT GAG AGC GAT Ser Glu Glu Glu Ser Glu Thr Glu Glu Glu Ser Glu Asp Glu Ser Asp 130 135 140 145	550
GAG GAG AGT GAA GAA GAC AGC GAG GAA GAA ATG GAG GAT GAG CAA GAA Glu Glu Ser Glu Glu Asp Ser Glu Glu Glu Met Glu Asp Glu Gln Glu 150 155 160	598
AGC GAG GCC GAA GAA GAC AAC CAA GAA GAA GGG GAA TCC GAG GCG GAG Ser Glu Ala Glu Glu Asp Asn Gln Glu Glu Gly Glu Ser Glu Ala Glu 165 170 175	646
GGA GAA ACT GAG GCA GAA AGT GAA TTT GAC CCA GAA ATA GAA ATG GAA Gly Glu Thr Glu Ala Glu Ser Glu Phe Asp Pro Glu Ile Glu Met Glu 180 185 190	694
GCA GAG AGA GTG GCC AAG AGG AAG TGT CCG GAC CAT GGG CTT GAT TTG Ala Glu Arg Val Ala Lys Arg Lys Cys Pro Asp His Gly Leu Asp Leu 195 200 205	742
AGT ACC TAT TGC CAG GAA GAT AGG CAG CTC ATC TGT GTC CTG TGT CCA Ser Thr Tyr Cys Gln Glu Asp Arg Gln Leu Ile Cys Val Leu Cys Pro 210 215 220 225	790
GTC ATT GGG GCT CAC CAG GGC CAC CAA CTC TCC ACC CTA GAC GAA GCC Val Ile Gly Ala His Gln Gly His Gln Leu Ser Thr Leu Asp Glu Ala 230 235 240	838
TTT GAA GAA TTA AGA AGC AAA GAC TCA GGT GGA CTG AAG GCC GCT ATG Phe Glu Glu Leu Arg Ser Lys Asp Ser Gly Gly Leu Lys Ala Ala Met 245 250 255	886
ATC GAA TTG GTG GAA AGG TTG AAG TTC AAG AGC TCA GAC CCT AAA GTA Ile Glu Leu Val Glu Arg Leu Lys Phe Lys Ser Ser Asp Pro Lys Val 260 265 270	934
ACT CGG GAC CAA ATG AAG ATG TTT ATA CAG CAG GAA TTT AAG AAA GTT Thr Arg Asp Gln Met Lys Met Phe Ile Gln Gln Glu Phe Lys Lys Val 275 280 285	982
CAG AAA GTG ATT GCT GAT GAG GAG CAG AAG GCC CTT CAT CTA GTG GAC Gln Lys Val Ile Ala Asp Glu Glu Gln Lys Ala Leu His Leu Val Asp 290 295 300 305	1030
ATC CAA GAG GCA ATG GCC ACA GCT CAT GTG ACT GAG ATA CTG GCA GAC	1078

Ile	Gln	Glu	Ala	Met	Ala	Thr	Ala	His	Val	Thr	Glu	Ile	Leu	Ala	Asp	
				310					315					320		
ATC	CAA	TCC	CAC	ATG	GAT	AGG	TTG	ATG	ACT	CAG	ATG	GCC	CAA	GCC	AAG	1126
Ile	Gln	Ser	His	Met	Asp	Arg	Leu	Met	Thr	Gln	Met	Ala	Gln	Ala	Lys	
			325					330					335			
GAA	CAA	CTT	GAT	ACC	TCT	AAT	GAA	TCA	GCT	GAG	CCA	AAG	GCA	GAG	GGC	1174
Glu	Gln	Leu	Asp	Thr	Ser	Asn	Glu	Ser	Ala	Glu	Pro	Lys	Ala	Glu	Gly	
		340					345					350				
GAT	GAG	GAA	GGA	CCC	AGT	GGT	GCC	AGT	GAA	GAA	GAG	GAC	ACA	TGA	AGGCTT	1225
Asp	Glu	Glu	Gly	Pro	Ser	Gly	Ala	Ser	Glu	Glu	Glu	Asp	Thr			
	355					360					365					
GCTACCCCCA	GTGGAAAATC	ATCCCTCCC	CTTGTGTGTA	TGTGACAGCG	TGTATGTAAC											1285
GGCTTCTGAT	TTCTGTGAAA	GCTGCTCAGC	AACAAACGTA	CTTCCACCAG	ATGTGTCCCC											1345
AGATCCACAG	CAGGCACATA	TCTCTCCAAG	GGATGACCAG	TTTTATGCTT	ACTGTGTGCT											1405
TCTCATCCCC	TGGTGTGGT	AGGTCAAGGA	AAAGAGCCCC	TTTGATCCAC	CAGGAGCAAT											1465
TAAGAAAGGT	CCTTCAGGTA	ATCCCTCAAT	GGCTGCTTTG	AACCTTACTCA	GGAAAGCCAG											1525
CCCCCATAAT	ATTGTATTAC	CAAACAGTAT	CGCTTTGTGA	GGAAGGATCT	GGAATAATCT											1585
TGAAGGGAAG	TCAGAGTTTT	CTCCCTGCCT	ATTAACAAAA	ACCCAATTTT	GTTCATATTG											1645
AAGCATGAAA	TAAATGAGAG	CAAGGTAGGG	CCAAATTAAC	TCTTGTGGAC	AGTCCCTAAA											1705
AGTCCAGTTC	TACATTTGTG	AAAATTGTGG	TGCCATGAAT	TAAGATGGAT	GAAGTGGAAA											1765
AGGTGTTGGA	GAAAGAGTTA	AAGATGAGGA	AGAGATATTT	TTAGTATATG	AAGTTATCCA											1825
GGACTTGATA	TTCATAATTC	AGTGCTGTGG	AAATGAAAAA	AATGATTGAA	GAGGTGGAAC											1885
GGAAATGACC	TTAGGGGGAA	AAAAAAGGAC	CAAAGAAGTC	TGATTAAAAG	TTGAAATCAG											1945
TATTTCTGAA	TTCAAATTGC	TTGAATTTC	AAAATAGTCA	GTAAGGATC	TAATAGAACC											2005
AGAATTATTT	GGGTGAATTC	TGCAGGTTTT	ATGGGCTTGT	CACAACGTGA	AGGGCTGGAA											2065
TGTATATTAC	CAAATGGGAA	TTTCCATTGT	AGGTTTTTGC	TAGTCCCACC	CCCATTTTAG											2125
CCTAATTTGG	CTTAAACGCA	GTATGGGGAG	AATTGTTCCC	ATTCCATGTG	TTCTGAATTC											2185
AGCTCATCTC	CCAGCATATA	GATATATCCT	CCTTTAACTC	CGACCAGAAC	CCTTCTTCCT											2245
GTGGCACTCC	CCACCCATAG	ACCTTCAGAT	CATCTCCAC	ACCCTGGATC	TCACTCTCCT											2305
CTTAGTAACA	GAGACACTCC	TGAGGTTGGA	CTTCTTGCT	TTTCTCTACT	TCCAAATCAC											2365
AATTTCTTAC	AACCAAGCTT	TGTGCTCCCG	AGTAAGCAGG	GATGTACTAG	GGGAATGTAA											2425
AACTGCAAAC	TTAAAAACCT	GCATCTTCTT	GAAGCATCAG	TTTTACTTAC	CAAATGGTTT											2485
AGAGTCATAA	GATGACCTAT	TTTTATATAA	AAGTTATATT	ATAGAATAAA	ATGTTCATAC											2545
GCATAGACTG	TTAAG															2560

<210> 173

<211> 367

<212> PRT

<213> Homo sapiens

173

Met	Arg	Pro	Arg	Gly	Arg	Lys	Ala	Ala	Ser	Pro	Gly	Ala	Pro	Arg	Pro	
1				5					10				15			
Trp	Pro	Arg	His	Ser	Thr	His	Met	Ala	Ser	Gly	Val	Gly	Ala	Ala	Phe	
			20					25					30			
Glu	Glu	Leu	Pro	His	Asp	Gly	Thr	Cys	Asp	Glu	Cys	Glu	Pro	Asp	Glu	
		35				40						45				
Ala	Pro	Gly	Ala	Glu	Glu	Val	Cys	Arg	Glu	Cys	Gly	Phe	Cys	Tyr	Cys	
	50					55					60					
Arg	Arg	His	Ala	Glu	Ala	His	Arg	Gln	Lys	Phe	Leu	Ser	His	His	Leu	

65		70		75		80									
Ala	Glu	Tyr	Val	His	Gly	Ser	Gln	Ala	Trp	Thr	Pro	Pro	Ala	Asp	Gly
				85					90					95	
Glu	Gly	Ala	Gly	Lys	Glu	Glu	Ala	Glu	Val	Lys	Val	Glu	Gln	Glu	Arg
			100					105					110		
Glu	Ile	Glu	Ser	Glu	Ala	Gly	Glu	Glu	Ser	Glu	Ser	Glu	Glu	Glu	Ser
		115					120					125			
Glu	Ser	Glu	Glu	Glu	Ser	Glu	Thr	Glu	Glu	Glu	Ser	Glu	Asp	Glu	Ser
	130					135					140				
Asp	Glu	Glu	Ser	Glu	Glu	Asp	Ser	Glu	Glu	Glu	Met	Glu	Asp	Glu	Gln
145					150					155				160	
Glu	Ser	Glu	Ala	Glu	Glu	Asp	Asn	Gln	Glu	Glu	Gly	Glu	Ser	Glu	Ala
			165					170						175	
Glu	Gly	Glu	Thr	Glu	Ala	Glu	Ser	Glu	Phe	Asp	Pro	Glu	Ile	Glu	Met
			180					185					190		
Glu	Ala	Glu	Arg	Val	Ala	Lys	Arg	Lys	Cys	Pro	Asp	His	Gly	Leu	Asp
		195					200					205			
Leu	Ser	Thr	Tyr	Cys	Gln	Glu	Asp	Arg	Gln	Leu	Ile	Cys	Val	Leu	Cys
	210				215					220					
Pro	Val	Ile	Gly	Ala	His	Gln	Gly	His	Gln	Leu	Ser	Thr	Leu	Asp	Glu
225				230					235					240	
Ala	Phe	Glu	Glu	Leu	Arg	Ser	Lys	Asp	Ser	Gly	Gly	Leu	Lys	Ala	Ala
			245					250						255	
Met	Ile	Glu	Leu	Val	Glu	Arg	Leu	Lys	Phe	Lys	Ser	Ser	Asp	Pro	Lys
		260					265						270		
Val	Thr	Arg	Asp	Gln	Met	Lys	Met	Phe	Ile	Gln	Gln	Glu	Phe	Lys	Lys
		275				280						285			
Val	Gln	Lys	Val	Ile	Ala	Asp	Glu	Glu	Gln	Lys	Ala	Leu	His	Leu	Val
	290				295						300				
Asp	Ile	Gln	Glu	Ala	Met	Ala	Thr	Ala	His	Val	Thr	Glu	Ile	Leu	Ala
305				310						315				320	
Asp	Ile	Gln	Ser	His	Met	Asp	Arg	Leu	Met	Thr	Gln	Met	Ala	Gln	Ala
				325						330				335	
Lys	Glu	Gln	Leu	Asp	Thr	Ser	Asn	Glu	Ser	Ala	Glu	Pro	Lys	Ala	Glu
			340					345						350	
Gly	Asp	Glu	Glu	Gly	Pro	Ser	Gly	Ala	Ser	Glu	Glu	Glu	Asp	Thr	
	355						360						365		

<210> 174

<211> 41

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of the artificial sequence:a synthetic DNA

<400> 174

ttaaagcttgc caccatgagc aaccccagcg cccaccacc a 41

<210> 175

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of the artificial sequence:a synthetic DNA

<400> 175

gtatcgattt aattgcatc ccccatcag 29

176

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of the artificial sequence:a synthetic DNA

<400> 176

cacctactglatgacaccacattc 24

<210> 177

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of the artificial sequence:a synthetic DNA

<400> 177

gagatgctgttccatgctggcctg 24

<210> 178

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of the artificial sequence:a synthetic DNA

<400> 178

ggaaagctctccgtggctaacaag 24

<210> 179

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of the artificial sequence:a synthetic DNA

<400> 179

catagtccttgacaagggtcacag 24

<210> 180

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of the artificial sequence:a synthetic DNA

<400> 180

cccatcaccatcttccaggagc

22

<210> 181

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of the artificial sequence:a synthetic DNA

<400> 181

ttcaccaccttcttgatgtcatcata

26